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OM protein - protein search, using sw model

Run on: February 13, 2004, 15:14:02 ; Search time 44 Seconds
(without alignments)
1230.131 Million cell updates/sec

Title: US-10-006-818A-77

Perfect score: 1816

Sequence: 1 MALPSRILLWLKVLQSSNV.....SPLPAKYIDLDKGRKENCK 341

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03.*

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- 2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
- 5: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
- 6: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
- 7: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
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- 10: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
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- 17: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
- 18: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
- 19: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
- 24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1816	100.0	341	21	Human PRO1293 prot
2	1816	100.0	341	21	Human PRO1293 (UNQ
3	1816	100.0	341	22	Protein of the inv
4	1755.5	96.7	442	22	Human protein havi
5	1755.5	96.7	442	24	Human SSCP-4 prote
6	1706	93.9	384	21	Human MTC48. Homo
7	1694.5	93.3	450	22	Human protein sequ
8	1367.5	75.3	442	23	Rat protein isolat
9	1362.5	75.0	442	22	Murine adipocytes-

10	1300	71.6	269	22	ABBI10350	Human cDNA SEQ ID
11	1300	71.6	269	23	ABP66937	Human polypeptide
12	1006	55.4	290	21	AAB59011	Breast and ovarian
13	955	52.6	192	22	ABBI0523	Human cDNA SEQ ID
14	955	52.6	192	22	AAU18028	Human immunoglobul
15	955	52.6	192	23	ABP67110	Human polypeptide
16	840	46.3	255	23	ABP72366	Murine protein iso
17	826.5	45.5	260	21	AAB36108	Mouse MTC48. Mus
18	355	19.5	218	24	ABP46671	Human SSCP-23 prot
19	127	7.0	447	24	ABR39440	Human GENSET poly
20	125.5	6.9	651	19	AAW62782	Protein encoded by
21	125	6.9	244	22	AAW62782	Human TF anti-idio
22	123	6.8	650	19	AAW62544	Human LIR-P3G2 pro
23	123	6.8	650	21	AAW62544	Leukocyte immunogl
24	122	6.7	253	23	ABP45328	Human Blys binding
25	122	6.7	652	19	AAW62545	Human LIR-18A3 pro
26	122	6.7	652	21	AAW62545	Leukocyte immunogl
27	121	6.7	254	23	ABP45955	Human Blys binding
28	120	6.6	266	23	ABP45955	Single chain antib
29	120	6.6	266	23	ABG35336	Thrombopoietin ago
30	119.5	6.6	246	21	AAW15126	Anti-murine CTLA-4
31	119.5	6.6	249	23	ABP45951	Human Blys binding
32	119	6.6	240	22	AAW6058	Human LIR-anti-idio
33	118.5	6.5	448	19	AAW62551	Human LIR-pb2 pro
34	118.5	6.5	448	19	AAW62551	Human gp49 HMI8 po
35	118.5	6.5	448	21	AAW62551	Leukocyte immunogl
36	118.5	6.5	469	22	AAW41582	Human polypeptide
37	117.5	6.5	472	19	AAW62334	FCR-IV protein seq
38	117	6.4	239	22	AAW6059	Human TF anti-idio
39	116.5	6.4	244	20	AAW6718	Antibody 12E10 sin
40	116.5	6.4	328	23	AAW6718	Cell adhesion mole
41	116	6.4	253	23	ABP45591	Human Blys binding
42	115.5	6.4	249	23	ABP45607	Human Blys binding
43	115.5	6.4	251	23	ABP45535	Human Blys binding
44	115.5	6.4	533	22	AAW33372	Human polypeptide,
45	115.5	6.4	534	22	AAW00906	Human B lymphocyte

ALIGNMENTS

RESULT 1
AAB24031
ID AAB24031 standard; Protein; 341 AA.
XX
AC AAB24031;
XX
DT 25-JAN-2001 (first entry)

XX Human PRO1293 protein sequence SEQ ID NO:31.

XX Human; tumour; diagnosis; neoplastic disease; proliferation; cancer;
XX Identification; tumorigenesis; anticancer; detection.

XX Homo sapiens.

XX WO200003750-A1.

XX 14-SEP-2000.

XX 02-DEC-1999; 99WO-US28551.

XX 08-MAR-1999; 99WO-US05028.

XX 01-SEP-1999; 99WO-US02011.

XX 29-OCT-1999; 99US-0182506.

XX 30-NOV-1999; 99WO-US28313.

XX 01-DEC-1999; 99WO-US28634.

XX (GETH) GENENTECH INC.

XX Botstein D, Goddard A, Gurney AL, Roy MA, Watanabe CK, Wood WI;

XX WFI; 2000-594320/56.

DR N-PSDB; AAC58113.
XX Antibodies specific for PRO polypeptides, used to diagnose and inhibit
PT the growth of tumors in mammals, and to identify inhibitors of PRO
PT polypeptide activity or expression.
XX Claim 61; Fig 22; 226pp; English.
XX
CC The present invention describes an antibody that binds to a human
CC protein (I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780;
CC PRO3434; PRO1297; PRO3567; PRO1293; PRO1303; PRO4344; PRO4354;
CC PRO4397; PRO4407; PRO1555; PRO1096; PRO2038; and PRO2262. (I) has
CC anticancer activity and can be used to diagnose tumours in mammals, by
CC detecting complex formation when the antibody is contacted with test
CC cells. Increased expression of genes encoding (I) can also be detected
CC to diagnose tumours. Agents which inhibit the activity of (I),
CC especially the antibodies, or an antisense oligonucleotide which
CC hybridises to genes encoding (I), can be used to inhibit tumour growth,
CC preferably by inducing cell death. Methods from the present invention
CC can be used to identify compounds which inhibit the biological activity
CC of (I). AAC58019 to AAC58102 represent PCR primers and hybridisation
CC probes used in examples from the present invention for human PRO
CC sequences. AAC58103 to AAC58122 and AAC58201 to AAC58240 represent human
CC PRO polynucleotide and protein sequences given in the exemplification of
CC the present invention.
XX
XX Sequence 341 AA;
SQ
Query Match 100.0%; Score 1816; DB 21; Length 341;
Best Local Similarity 100.0%; Fred. No. 4.8e-155; Mismatches 0; Gaps 0;
Matches 341; Conservative 0; Indels 0;
QY 1 MALPSRILLKVLQSSAVLLHSAVEETDAGLYTCNLHHYCHLYESLAVLEVTGPP 60
Db 1 MALPSRILLKVLQSSAVLLHSAVEETDAGLYTCNLHHYCHLYESLAVLEVTGPP 60
QY 61 ATPAYDGEKEVLAVARGAPALLTCVNRGHVWTDHVEEAQVWHDROPVGPVDRADR 120
Db 61 ATPAYDGEKEVLAVARGAPALLTCVNRGHVWTDHVEEAQVWHDROPVGPVDRADR 120
QY 121 LLDLYASGERRAYGPIFLDRVAVGADAFERGDFSLRIEPLFVADGTYSCHLHHYCG 180
Db 121 LLDLYASGERRAYGPIFLDRVAVGADAFERGDFSLRIEPLFVADGTYSCHLHHYCG 180
QY 181 HERRVHLTVAEPAHPPRGSGNGSSHGAPGDPPTLARGHNVINIVPESRAHFFQ 240
Db 181 HERRVHLTVAEPAHPPRGSGNGSSHGAPGDPPTLARGHNVINIVPESRAHFFQ 240
QY 241 LGVVLATLLFILLVTLAARRRGVEYSQKSGKGDVNLAEFAVAGDQMLYR 300
Db 241 LGVVLATLLFILLVTLAARRRGVEYSQKSGKGDVNLAEFAVAGDQMLYR 300
QY 301 SEDIQDYKNNILKRAELAHSPKPYIDLDKGFRENCK 341
Db 301 SEDIQDYKNNILKRAELAHSPKPYIDLDKGFRENCK 341
RESULT 2
AAC59362
ID AAY99362 standard; Protein; 341 AA.
XX
AC AAY99362;
XX
DT 08-AUG-2000 (first entry)
XX
DE Human PRO1293 (UNQ652) amino acid sequence SEQ ID NO:77.
XX
KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
KW transmembrane; secretion; immunoadhesion; pharmaceutical; screening.
XX
OS Homo sapiens.
XX
FN WO200012708-A2.

XX 09-MAR-2000.
PD
XX 01-SEP-1998; 98US-0098716.
XX 01-SEP-1998; 98US-0098749.
XX 01-SEP-1998; 98US-0098750.
XX 02-SEP-1998; 98US-0098803.
XX 02-SEP-1998; 98US-0098821.
XX 02-SEP-1998; 98US-0098843.
XX 02-SEP-1998; 98US-0098936.
XX 09-SEP-1998; 98US-0099596.
XX 09-SEP-1998; 98US-0099598.
XX 09-SEP-1998; 98US-0099602.
XX 09-SEP-1998; 98US-0099642.
XX 10-SEP-1998; 98US-0099741.
XX 10-SEP-1998; 98US-0099754.
XX 10-SEP-1998; 98US-0099763.
XX 10-SEP-1998; 98US-0099792.
XX 10-SEP-1998; 98US-0099808.
XX 10-SEP-1998; 98US-0099812.
XX 10-SEP-1998; 98US-0099815.
XX 10-SEP-1998; 98US-0099816.
XX 15-SEP-1998; 98US-0100385.
XX 15-SEP-1998; 98US-0100388.
XX 15-SEP-1998; 98US-0100390.
XX 16-SEP-1998; 98US-0100584.
XX 16-SEP-1998; 98US-0100627.
XX 16-SEP-1998; 98US-0100661.
XX 16-SEP-1998; 98US-0100662.
XX 16-SEP-1998; 98US-0100664.
XX 17-SEP-1998; 98US-0100683.
XX 17-SEP-1998; 98US-0100684.
XX 17-SEP-1998; 98US-0100710.
XX 17-SEP-1998; 98US-0100711.
XX 17-SEP-1998; 98US-0100919.
XX 17-SEP-1998; 98US-0100930.
XX 18-SEP-1998; 98US-0100848.
XX 18-SEP-1998; 98US-0100849.
XX 18-SEP-1998; 98US-0101014.
XX 18-SEP-1998; 98US-0101068.
XX 18-SEP-1998; 98US-0101071.
XX 22-SEP-1998; 98US-0101279.
XX 23-SEP-1998; 98US-0101471.
XX 23-SEP-1998; 98US-0101472.
XX 23-SEP-1998; 98US-0101474.
XX 23-SEP-1998; 98US-0101475.
XX 23-SEP-1998; 98US-0101476.
XX 23-SEP-1998; 98US-0101477.
XX 23-SEP-1998; 98US-0101479.
XX 24-SEP-1998; 98US-0101738.
XX 24-SEP-1998; 98US-0101741.
XX 24-SEP-1998; 98US-0101743.
XX 24-SEP-1998; 98US-0101915.
XX 29-SEP-1998; 98US-0101916.
XX 29-SEP-1998; 98US-0102207.
XX 29-SEP-1998; 98US-0102240.
XX 29-SEP-1998; 98US-0102307.
XX 29-SEP-1998; 98US-0102330.
XX 29-SEP-1998; 98US-0102331.
XX 30-SEP-1998; 98US-0102484.
XX 30-SEP-1998; 98US-0102487.
XX 30-SEP-1998; 98US-0102570.
XX 30-SEP-1998; 98US-0102571.
XX 01-OCT-1998; 98US-0102684.
XX 01-OCT-1998; 98US-0102687.
XX 02-OCT-1998; 98US-0102965.
XX 06-OCT-1998; 98US-0103258.
XX 06-OCT-1998; 98US-0103449.
XX 07-OCT-1998; 98US-0103314.
XX 07-OCT-1998; 98US-0103315.
XX 07-OCT-1998; 98US-0103328.

XX WPI; 2001-071395/08.
 DR Secreted and transmembrane proteins and nucleic acids designated PRO,
 PT usefull as hybridization probes, in chromosome and gene mapping and gene
 PT therapy -
 XX
 PS Claim 1; Fig 46; 787pp; English.
 XX
 CC The present invention relates to secreted and transmembrane proteins.
 CC These proteins and the DNA encoding them may be used as hybridization
 CC probes, in chromosome and gene mapping and in the generation of
 CC anti-sense RNA and DNA. They may also be used to generate either
 CC transgenic animals or knockout animals which are in turn useful for
 CC development and screening of therapeutically useful reagents.
 CC The nucleic acids may also be used in gene therapy.
 XX
 SQ Sequence 341 AA;
 Query Match 100.0%; Score 1816; DB 22; Length 341;
 Best Local Similarity 100.0%; Pred. No. 4.8e-155;
 Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MALPSRILLWKLVLLQSSAVLLHSVAEETDAGLYTCNLHHYCHLYESLAVLEVTGPP 60
 DB 1 MALPSRILLWKLVLLQSSAVLLHSVAEETDAGLYTCNLHHYCHLYESLAVLEVTGPP 60
 QY 61 ATPAYWGEKEVLAVARGAPALITCVNRGHVWTDHVEEAQVVDROPVPHDRADR 120
 DB 61 ATPAYWGEKEVLAVARGAPALITCVNRGHVWTDHVEEAQVVDROPVPHDRADR 120
 QY 121 LLDLYASGERAYGPLELDRVAVGADAFERGFSLRIEPLFVADGTYSCHLHHYCG 180
 DB 121 LLDLYASGERAYGPLELDRVAVGADAFERGFSLRIEPLFVADGTYSCHLHHYCG 180
 QY 181 HERVPHLTVAEPHAEPPRGSGSSGAPGDPPTLARGHNVINIVPESRAHFFQ 240
 DB 181 HERVPHLTVAEPHAEPPRGSGSSGAPGDPPTLARGHNVINIVPESRAHFFQ 240
 QY 241 LGYVLTATLLFILLVTLVLAARRRGVYEQSKGSKGVNLAEPFAVAGQMLYR 300
 DB 241 LGYVLTATLLFILLVTLVLAARRRGVYEQSKGSKGVNLAEPFAVAGQMLYR 300
 QY 301 SEDIQLDYKNILKERAEHLAHSPLPAKYIDLKGFKECK 341
 DB 301 SEDIQLDYKNILKERAEHLAHSPLPAKYIDLKGFKECK 341
 RESULT 4
 ID AAE06578 standard; Protein; 442 AA.
 AC AAE06578;
 XX
 DT 25-SEP-2001 (first entry)
 XX
 DE Human protein having hydrophobic domain, HP10769.
 XX
 KW Human; hydrophobic domain; gene therapy; nutritional supplement;
 KW cell proliferation; immunomodulatory; autoimmune disorder; antimicrobial;
 KW multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes;
 KW haematopoiesis; tissue growth activity; Parkinson's disease; cytostatic;
 KW Huntington's disease; Alzheimer's disease; chemotactic; chemokinetic;
 KW haemostatic; thrombolytic; tumour growth inhibitor; anabolic;
 KW contraceptive; antiinfertility; antiinflammatory.
 XX
 OS Homo sapiens.
 XX
 FN W0200149728-A2.
 XX
 PD 12-JUL-2001.
 XX
 EF 28-DEC-2000; 2000WO-JP09359.

XX 06-JAN-2000; 2000JP-0000585.
 PR 06-JAN-2000; 2000JP-0000588.
 PR 11-JAN-2000; 2000JP-0002299.
 PR 03-FEB-2000; 2000JP-0026862.
 PR 03-MAR-2000; 2000JP-0058367.
 XX
 PA (PROT-) PROTEGENE INC.
 PA (SAGA) SAGAMI CHEM RES CENT.
 XX
 PI Kato S, Kimura T;
 XX WPI; 2001-418355/44.
 DR N-PSDB; AAD12573.
 XX
 PT Human proteins with hydrophobic domains and the nucleic acids encoding
 PT them, useful for preventing diagnosing and treating e.g. cancer,
 PT Alzheimer's and inflammation -
 XX
 XX Claim 1; Page 236-238; 563pp; English.
 PS The present sequence is human protein with hydrophobic domain,
 CC HP10769. The polynucleotide and polypeptide of the invention
 CC may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate polypeptide expression. The polynucleotides
 CC may be used to produce the polypeptide by inserting the nucleic acids
 CC into a host cell and culturing the cell to express the protein. The
 CC polynucleotides and its complementary sequences may also be used as DNA
 CC probes in diagnostic assays and also used in gene therapy. The
 CC polypeptides may also be used as antigens in the production of antibodies
 CC and in assays to identify modulators of polypeptide expression and
 CC activity. The polypeptides and nucleic acids may be used as nutritional
 CC supplements, to modulate cytokine and cell proliferation activity, to
 CC modulate immune stimulation or suppression (e.g. for the treatment of
 CC microbial infections and autoimmune disorders such as multiple sclerosis,
 CC rheumatoid arthritis and insulin-dependent diabetes), to modulate
 CC haematopoiesis, to modulate tissue growth activity (e.g. for the
 CC treatment of Parkinson's disease, Huntington's disease and Alzheimer's
 CC disease), to modulate activin and inhibin activity (e.g. for controlling
 CC fertility), to modulate chemotactic and chemokinetic activity, to
 CC modulate haemostatic and thrombolytic activity, to modulate receptor
 CC ligand activity, to modulate inflammation and to inhibit tumour growth.
 XX
 SQ Sequence 442 AA;

Query Match 96.7%; Score 1755.5; DB 22; Length 442;
 Best Local Similarity 77.1%; Pred. No. 1.8e-149;
 Matches 341; Conservative 0; Mismatches 0; Indels 101; Gaps 1;
 QY 1 MALPSRILLWKLVLLQSSAVLLHS----- 24
 DB 1 MALPSRILLWKLVLLQSSAVLLHSQSSVPAAGSSVSVSESAVSEAGARAVLRQSPMV 60
 QY 25 ----- 24
 DB 61 WTQDLRHQRVLRHWDLRGPGGFPARRLLDLYSAGEQVYEARDGRLELSASAFDDGNF 120
 QY 25 -----AVEETDAGLYTCNLHHYCHLYESLAVLEVTGPPATPAYWDGEKVLAVARGA 79
 DB 121 SLLIRAVEETDAGLYTCNLHHYCHLYESLAVLEVTGPPATPAYWDGEKVLAVARGA 180
 QY 80 PALLTCVNRGHVWTDHVEEAQVVDROPVPHDRADRLLDLYASGERAYGPLEFLR 139
 DB 181 PALLTCVNRGHVWTDHVEEAQVVDROPVPHDRADRLLDLYASGERAYGPLEFLR 240
 QY 140 DRVAVGADAFERGFSLRIEPLFVADGTYSCHLHHYCHLYESLAVLEVTGPPATPAYWDGEKVLAVARGA 199
 DB 241 DRVAVGADAFERGFSLRIEPLFVADGTYSCHLHHYCHLYESLAVLEVTGPPATPAYWDGEKVLAVARGA 300
 QY 200 RQSPNGSSSHGAPGDPPTLARGHNVINIVPESRAHFFQQLGYVLTATLLFILLVTL 259
 DB 301 RQSPNGSSSHGAPGDPPTLARGHNVINIVPESRAHFFQQLGYVLTATLLFILLVTL 360

QY 260 LAARRRGVEYSQKSGKGVNLAFAVAAGDQMLYRSEDQLDYKNILKRAEL 319
 DB 361 LAARRRGVEYSQKSGKGVNLAFAVAAGDQMLYRSEDQLDYKNILKRAEL 420
 QY 320 AHSPLPAKYIDLKGRKENCK 341
 DB 421 AHSPLPAKYIDLKGRKENCK 442

RESULT 5

ABB84652
 ID ABB84652 standard; Protein; 442 AA.

AC ABB84652;

DT 11-FEB-2003 (first entry)

XX Human SSCP-4 protein from clone 1345785CD1 SEQ ID 4.

XX Secreted protein; SSCP; human; antiarteriosclerotic; antiatherosclerotic;
 KW hepatotropic; cytostatic; anti-HIV; antiallergic; antiasthmatic; cancer;
 KW antianaemic; antidiabetic; antiinflammatory; neuroprotective; antiulcer;
 KW antirheumatic; antiarthritic; cardiac; hypotensive; gonadal dysgenesis;
 KW vasotropic; anticonvulsant; nootropic; immunosuppressive; pericarditis;
 KW antiparkinsonian; ophthalmological; cell proliferative disorder;
 KW arteriosclerosis; atherosclerosis; cirrhosis; hepatitis; angina pectoris;
 KW autoimmune disorder; AIDS; Crohn's disease; multiple sclerosis; epilepsy;
 KW ulcerative colitis; cardiovascular disorder; myocardial infarction;
 KW Raynaud's disease; myocarditis; neurological disorder; cataract;
 KW Huntington's disease; Alzheimer's disease; Creutzfeldt-Jakob disease;
 KW developmental disorder; Duchenne muscular dystrophy; antipsoriatic;
 KW Becker muscular dystrophy; Cushing's syndrome.

XX Homo sapiens.

XX WC200279441-A2.

XX 10-OCT-2002.

XX 29-MAR-2002; 2002WO-US09820.

XX 30-MAR-2001; 2001US-280527P.

XX 06-APR-2001; 2001US-282112P.

XX 09-APR-2001; 2001US-282702P.

XX 13-APR-2001; 2001US-283855P.

XX 19-OCT-2001; 2001US-343718P.

XX 07-DEC-2001; 2001US-339236P.

XX 13-FEB-2002; 2002US-357002P.

XX (INCY-) INCYTE GENOMICS INC.

XX Baughn MR, Burford N, Ding L, Duggan BM, Elliott VS, Forsythe LJ;
 PI Gandhi AR, Gietzen KU, Griffin JA, He A, Honchell CD, Ison CH;
 PI Lal PG, Lee EA, Lee S, Lu DAM, Mason PM, Sanjanwala MM;
 PI Swarnakar A, Rankumar J, Tang YT, Thangavelu K, Tran UK, Walia NK;
 PI Warren BA, Yao MG, Xu Y, Yue H;

XX WPI; 2003-058429/05.

DR N-PSDB; ABB57548.

XX Novel human secreted protein useful for treating, preventing or
 PT diagnosing cancer, hepatitis, psoriasis, asthma, diabetes mellitus,
 PT anemia, epilepsy, cataract, Alzheimer's disease

XX Claim 59; Page 152-153; 188pp; English.

XX This invention describes novel secreted proteins (SECP) which have
 CC antiarteriosclerotic, antiatherosclerotic, hepatotropic, cytostatic,
 CC anti-HIV, antiallergic, antiasthmatic, antianaemic, antidiabetic,
 CC antiinflammatory, neuroprotective, antiulcer, antipsoriatic, vasotropic,
 CC antirheumatic, antiarthritic, cardiac, hypotensive, anticonvulsant,
 CC nootropic, immunosuppressive, antiparkinsonian and ophthalmological
 CC activity. The polynucleotides and polypeptides of the invention can be

CC used for diagnosing, treating or preventing cell proliferative disorder
 CC e.g. arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, cancer
 CC autoimmune/inflammatory disorders e.g. acquired immunodeficiency syndrome
 CC (AIDS), allergies, asthma, anaemia, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, ulcerative colitis, psoriasis, rheumatoid arthritis,
 CC etc; cardiovascular disorder e.g. myocardial infarction, angina pectoris,
 CC hypertension, Raynaud's disease, myocarditis, pericarditis, etc;
 CC neurological disorders e.g. epilepsy, Huntington's disease, Parkinson's
 CC disease, Alzheimer's disease, Creutzfeldt-Jakob disease, etc; and
 CC developmental disorders e.g. Duchenne and Becker muscular dystrophy,
 CC cataract, gonadal dysgenesis, Cushing's syndrome, etc. The products of
 CC the invention can also be used for drug screening, proteome analysis, to
 CC microarrays creating knock-in humanised animals or transgenic animals to
 CC model human diseases, in somatic or germline gene therapy, to generate a
 CC transcript image of a tissue or cell type, for detecting differences in
 CC the chromosomal location due to translocation, inversion, etc., among
 CC normal, carrier or affected individuals, and as hybridization probes for
 CC mapping naturally occurring genomic sequences ABB84649-ABB84673
 CC represent secreted proteins encoded by the cDNA's shown in
 CC ABB57545-ABB57569, described in the disclosure of the invention.

XX Sequence 442 AA;

Query Match 96.7%; Score 1755.5; DB 24; Length 442;

Best Local Similarity 77.1%; Pred No. 1.8e-149;

Matches 341; Conservative 0; Mismatches 0; Indels 101; Gaps 1;

QY 1 MALPSRILLKVLQSSAVLLHS----- 24

DB 1 MALPSRILLKVLQSSAVLLHSGSVPAAGSSVSVESAVSWEAGARAVLRQSPRMV 60

QY 25 ----- 24

DB 61 WTQRLHQRVLRHLDLRGCGGPARLLDLYSAGEORVTEARDGRLELSASAFDDGNF 120

QY 25 -----AVEETDAGLYTCNLHHYCHLYESLAVRLEVTGPPATPAYWDGKEVLAVARGA 79

DB 121 SLLTRAVEETDAGLYTCNLHHYCHLYESLAVRLEVTGPPATPAYWDGKEVLAVARGA 180

QY 80 PALLTCVNRGHVWTDRIHVEEAQVWHDROPVGVPHDRADRLDLYASGERRAYGFLR 139

DB 181 PALLTCVNRGHVWTDRIHVEEAQVWHDROPVGVPHDRADRLDLYASGERRAYGFLR 240

QY 140 DRVAVGADAFERGFSLRIEPLVADGTYSCHLHHYCGLHERRVPHLTVAEPHAEPPPP 199

DB 241 DRVAVGADAFERGFSLRIEPLVADGTYSCHLHHYCGLHERRVPHLTVAEPHAEPPPP 300

QY 200 RGSFNGSSSHSGAPGPDPTLARGHNVINIVPEGRAHFFQOLGVYLATLLLFILLVTVL 259

DB 301 RGSFNGSSSHSGAPGPDPTLARGHNVINIVPEGRAHFFQOLGVYLATLLLFILLVTVL 360

QY 260 LAARRRGVEYSQKSGKGVNLAFAVAAGDQMLYRSEDQLDYKNILKRAEL 319

DB 361 LAARRRGVEYSQKSGKGVNLAFAVAAGDQMLYRSEDQLDYKNILKRAEL 420

QY 320 AHSPLPAKYIDLKGRKENCK 341

DB 421 AHSPLPAKYIDLKGRKENCK 442

RESULT 6

AAB36107

ID AAB36107 standard; Protein; 384 AA.

XX AAB36107;

XX 20-FEB-2001 (first entry)

XX Human MTC48.

XX Human; cytostatic; metastatic thyroid cancer; MTC; thyroid carcinoma.

XX Homo sapiens.

OS

XX WO200063438-A2.
XX 26-OCT-2000.
XX 20-APR-2000; 2000WO-US10729.
XX 20-APR-1999; 99US-0130123.
XX 30-MAR-2000; 2000US-0193203.
XX 19-APR-2000; 2000US-0552322.
XX (CURA-) CURAGEN CORP.
XX
XX Gould-Rothberg BE, Rastelli L;
XX WPI; 2000-665252/64.
XX N-PSDB; AAC67985.
XX
XX Categorizing, diagnosing or assessing the prognosis of thyroid
XX carcinoma by measuring the expression levels of MTC (metastatic thyroid
XX cancer) genes -
XX
XX Disclosure; Page 33; 105pp; English.
XX
XX The present sequence is a novel metastatic thyroid cancer (MTC)
XX protein. A method of categorizing, diagnosing or assessing the prognosis
XX of thyroid carcinoma by measuring the expression levels of MTC genes is
XX disclosed. The MTC genes are differentially expressed in metastatic
XX thyroid cancer when compared to non-metastatic thyroid cancer. An
XX agent that decreases the expression or activity of one or more MTC genes
XX may be administered to treat metastatic carcinoma. Allele-specific
XX oligonucleotide probes that hybridize to an MTC polynucleotide at a
XX polymorphic site may be used to determine whether a subject suffers from
XX or is at risk of metastatic thyroid carcinoma.
XX
XX Sequence 384 AA;
XX
XX Query Match 93.9%; Score 1706; DB 21; Length 384;
XX Best Local Similarity 99.4%; Pred. No. 4.4e-145;
XX Matches 319; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 21 LLSAVEETDAGLYTCNLHHYCHLYESLAVRLEVTGPPATPAWDGKEVLAVARGAP 80
XX 64 LLIRAVEETDAGLYTCNLHHYCHLYESLAVRLEVTGPPATPAWDGKEVLAVARGAP 123
XX 81 ALLTCVNRGHVWTDHVEEAQQVHWDRQPPGVPHDRADRLDLVSGERRAYGFLFLRD 140
XX 124 ALLTCVNRGHVWTDHVEEAQQVHWDRQPPGVPHDRADRLDLVSGERRAYGFLFLRD 183
XX 141 RVAVGADAFERGFSLRIEPLFVADGTYSCHLHHYCHLHRRVFLTVAPHAEPFPPR 200
XX 184 RVAVGADAFERGFSLRIEPLFVADGTYSCHLHHYCHLHRRVFLTVAPHAEPFPPR 243
XX 201 GSPGNGSSHGAPGPDPTLARGHNVINIVPSRAHFFQOLGYVLATLLFLFILLVTVLL 260
XX 244 GSPGNGSSHGAPGPDPTLARGHNVINIVPSRAHFFQOLGYVLATLLFLFILLVTVLL 303
XX 261 AARRRGGEYSQKSGKGDVNLAEFAVAGDQMLYRSEDQLDYKNILKERAEIA 320
XX 304 AARRRGGEYSQKSGKGDVNLAEFAVAGDQMLYRSEDQLDYKNILKERAEIA 363
XX 321 HSPLPAKYIDLDKGRKENCK 341
XX 364 HSPLPAKYIDLDKGRKENCK 384
XX
XX RESULT 7
XX AAB92464
XX ID AAB92464 standard; Protein; 450 AA.
XX AC AAB92464;
XX DT 26-JUN-2001 (first entry)

XX Human protein sequence SEQ ID NO:10520.
XX Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX Homo sapiens.
XX EP1074617-A2.
XX 07-FEB-2001.
XX 28-JUL-2000; 2000EP-0116126.
XX 29-JUL-1999; 99JP-0248036.
XX 27-AUG-1999; 99JP-0300253.
XX 11-JAN-2000; 2000JP-0118776.
XX 02-MAY-2000; 2000JP-0183767.
XX 09-JUN-2000; 2000JP-0241899.
XX (HELI-) HELIX RES INST.
XX Ota T, Isegai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
XX Tshii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX WPI; 2001-318749/34.
XX
XX Primer sets for synthesizing polynucleotides, particularly the 5602
XX full-length cDNAs defined in the specification, and for the detection
XX and/or diagnosis of the abnormality of the proteins encoded by the
XX full-length cDNAs -
XX
XX Claim 8; SEQ ID 10520; 2537pp + CD ROM; English.
XX
XX The present invention describes primer sets for synthesizing 5602
XX full-length cDNAs defined in the specification. Where a primer set
XX comprises: (a) an oligo-dr primer and an oligonucleotide complementary
XX to the complementary strand of a polynucleotide which comprises one of
XX the 5602 nucleotide sequences defined in the specification, where the
XX oligonucleotide comprises at least 15 nucleotides; or (b) a combination
XX of an oligonucleotide comprising a sequence complementary to the
XX complementary strand of a polynucleotide which comprises a 5'-end
XX sequence and an oligonucleotide comprising a sequence complementary to a
XX polynucleotide which comprises a 3'-end sequence, where the
XX oligonucleotide comprises at least 15 nucleotides and the combination
XX of the 5'-end sequence/3'-end sequence is selected from those defined in
XX the specification. The primer sets can be used in antisense therapy and
XX in gene therapy. The primers are useful for synthesizing polynucleotides,
XX particularly full-length cDNAs. The primers are also useful for the
XX detection and/or diagnosis of the abnormality of the proteins encoded by
XX the full-length cDNAs. The primers allow obtaining of the full-length
XX cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
XX AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
XX AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
XX represent oligonucleotides, all of which are used in the exemplification
XX of the present invention.
XX
XX Sequence 450 AA;
XX
XX Query Match 93.3%; Score 1694.5; DB 22; Length 450;
XX Best Local Similarity 75.5%; Pred. No. 5.8e-144;
XX Matches 332; Conservative 1; Mismatches 0; Indels 107; Gaps 2;
XX
XX 1 MALPSRILLWKLVLQSSAVLLHS----- 24
XX 1 MALPSRILLWKLVLQSSAVLLHSGSVPAAGSSVVSESASVWEAGARAVLRCQSPMV 60
XX 25 ----- 24
XX 61 WTQRLHQRQVRLHWDLRPGGGPARLLDLYSAGEQRVYEARDRGRLELSASAFDDGNF 120
XX 25 -----AVEETDAGLYTCNLHHYCHLYESLAVRLEVTGPPATPAWDGKEVLAVARGA 79
XX 121 SLLIRAVEETDAGLYTCNLHHYCHLYESLAVRLEVTGPPATPAWDGKEVLAVARGA 180

QY 80 PALLTCVNRGHVWTDHRVEAQQVHVHWDROPVPHDRADRLDLYASGERRAYGFLFLR 139
DB 181 PALLTCVNRGHVWTDHRVEAQQVHVHWDROPVPHDRADRLDLYASGERRAYGFLFLR 240
QY 140 DRVAVGADAFERGFSLRIEPLFVADGTYSCHLHHYCGLHERRVFLHTVAEPHAEPPP 199
DB 241 DRVAVGADAFERGFSLRIEPLFVADGTYSCHLHHYCGLHERRVFLHTVAEPHAEPPP 300
QY 200 RGSFGNGSSHGAPGDPPTLARGHNVINIVPESRAHFQOOLGYVATLILLFILLVTVL 259
DB 301 RGSFGNGSSHGAPGDPPTLARGHNVINIVPESRAHFQOOLGYVATLILLFILLVTVL 360
QY 260 LAARRRGGEYSDQSGKSGKDVNLAEPFAVAAGDQMLYRSEDIOQ-----DYKNIL 313
DB 361 LAARRRGGEYSDQSGKSGKDVNLAEPFAVAAGDQMLYRSEDVQLASSPPPTDYKNIL 420
QY 314 KERAELAHSPKPYIDLDK 333
DB 421 KERAELAHSPKPYIDLDK 440

RESULT 8

AB872335
ID ABB72335 standard; Protein; 442 AA.

XX AC ABB72335;

DT 04-APR-2002 (first entry)

DE Rat protein isolated from skin cells SEQ ID NO: 659.

KW Human; rat; mouse; skin cell; skin wound; cancer; growth defect;
KW developmental defect; inflammatory disease; dermatological; vulnary;
KW immunomodulator; anti-inflammatory; cytostatic; neuroprotective.

OS Rattus sp.

XX PN W0200190357-Al.

XX PD 29-NOV-2001.

XX PF 24-MAY-2001; 2001WO-NZ00099.

XX PR 24-MAY-2000; 2000US-206650P.

XX PR 25-JUL-2000; 2000US-221232P.

XX PA (GENE-) GENESIS RES & DEV CORP LTD.

XX PI Watson JD, Strachan L, Sleeman M, Onrust R, Murison JG, Kumble KD;

XX DR WPI; 2002-122020/15.

XX DR N-PSDB; ABL3502L.

XX New polynucleotides and polypeptides encoded by the polynucleotides
PT isolated from skin cells, useful for treating skin wounds, cancers,
PT growth and developmental defects, inflammatory diseases, or for
PT modulating immune responses

XX Claim 4; Page 416-417; 466pp; English.

XX The present invention provides the protein and coding sequences of cDNAs
CC isolated from human, murine and rat skin cell libraries. The sequences
CC can be used in the development of therapeutic agents useful in the
CC treatment of skin diseases, including skin wounds, cancer, growth
CC defects, developmental defects and inflammatory diseases. The proteins
CC have important roles in the induction of hair growth, cell proliferation
CC and cell-cell interaction, in maintaining tissue integrity, in wound
CC healing and in modulating immune responses. The present sequence is a
CC polypeptide of the invention.

XX Sequence 442 AA;

Query Match 75.3%; Score 1367.5; DB 23; Length 442;

Best Local Similarity 61.3%; Fred. No. 1.5e-114; Indels 101; Gaps 3;
Matches 271; Conservative 22; Mismatches 48;

QY 1 MALPSRILLWKLVLQSSAVL----- 21
DB 1 MELLRSVLLWKLVLQSSAVLSSGSGPTAAASSSVSESVAAGTQAVLRCCSPRMV 60
QY 22 -----LHS----- 24
DB 61 TODRLHDEQRVHVHWDLSGGPGSGRRLLVDMYSAGEQRYVQPRDRRLLLSPSAFHDGNFS 120
QY 25 -----AVEETDAGLTCNLHHYCHLYESLAVRLEVTGPPATPAYWDGEKEVLAVARGAP 80
DB 121 LLIRAVERGDEGVTCNLHHYCHLYESLAVRLEVTDDPILLSRAYWDGEKEVLVVALGAP 180
QY 81 ALLTCVNRGHVWTDHRVEAQQVHVHWDROPVPHDRADRLDLYASGERRAYGFLFLR 140
DB 181 ALMTCVNREHLWTDRLHEAQQVHVHWDROPVPHDRADRLDLYASGERRAYGFLFLR 240
QY 141 RVAVGADAFERGFSLRIEPLFVADGTYSCHLHHYCGLHERRVFLHTVAEPHAEPPP 200
DB 241 RSVNTNFAFGDFSLRIDDLPEADGTYSCHLHHYCGLHERRVFLHTVAEPHAEPPP 300
QY 201 GSPNGSSHGAPGDPPTLARGHNVINIVPESRAHFQOOLGYVATLILLFILLVTVL 260
DB 301 ASPNGSGHNSVPSPDPTMARGHSIINVIVPEDHTFFQOLGYVATLILLFILLVTVL 360
QY 261 AARRR-GGYEYSDQSGKSGKDVNLAEPFAVAAGDQMLYRSEDIQLDYKNILKERAEL 319
DB 361 ATRHSGGCKTSRKGKSGKDVNMEFAIATRDQAPRTEDIQLDYKNILKERAEL 420
QY 320 AHSPLPAKYIDLDKGRKENC 341
DB 421 AHSPLPAKVDLDKFRKCYCK 442

RESULT 9

AA85860
ID AA85860 standard; Protein; 442 AA.

XX AC AA85860;

XX DT 30-NOV-2001 (first entry)

XX DE Murine adipocytes-derived protein.

XX KW Adipocyte; murine; differentiation; obesity; hyperlipemia; diabetes;
XX atherosclerosis.

XX OS Mus musculus.

XX PN W0200166720-Al.

XX PD 13-SEP-2001.

XX PF 09-MAR-2001; 2001WO-JP01863.

XX PR 10-MAR-2000; 2000JP-0072502.

XX PA (KITA/) KITAMURA T.

XX PA (TSUR/) TSURUGA H.

XX PI Kitamura T, Tsuruga H;

XX DR WPI; 2001-565585/63.

XX DR N-PSDB; AAH76374.

XX Genes associated with adipocyte differentiation for screening
PT adipocyte-related disorders such as diabetes and hyperlipemia

XX Claim 1; Page 85-88; 112pp; Japanese.

CC The invention relates to genes derived from murine adipocytes and
 CC proteins encoded by these genes. The proteins are associated with
 CC adipocyte differentiation and can be expressed by standard recombinant
 CC methodology. The genes, proteins and specific antibodies are useful for
 CC the identification of drugs for treatment and prevention of adipocyte-
 CC related disorders such as obesity, hyperlipemia, diabetes and
 CC atherosclerosis. The present sequence represents a protein encoded by
 CC the gene derived from murine adipocytes.

XX
 SQ Sequence 442 AA;

Query Match 75.0%; Score 1362.5; DB 22; Length 442;
 Best Local Similarity 61.3%; Pred. No. 4.3e-114;
 Matches 271; Conservative 21; Mismatches 49; Indels 101; Gaps 3;

Qy 1 MALPSRILLKIVLLQSSAVL----- 21
 Db 1 MELLRSVLLKLLQSSAVL----- 60
 Qy 22 ----LHS----- 24
 Db 61 TQRLHQRVHWDLSGGPGSORRELVDVMSAGEGRVYPRDRLLLSPSAPHDGNFS 120
 Qy 25 ----AVETDAGLYTNLHHYCHLYESLAVLEVTDPPTATPVAWDGEKEVLAVAGAP 80
 Db 121 LLIRAVERGEGYTCNLHHYCHLDESIAVLEVTEDPLLSRAYWDGEKEVLVVAHGAP 180
 Qy 81 ALLTCVNRGHVWTDREVEEAQVHVWDROPVGPVHDRAADRLLDLYASGERRAYGFLFIRD 140
 Db 181 ALMTCINRAHVWTDREHLEEAQVHVWDROLPGVSHDRAADRLLDLYASGERRAYGFPFLRD 240
 Qy 141 RVAVGADAFERGQPSLRLEPLEVDEGTYSCHLHHYCHLHRRVPHLTVAPPAEPFPPR 200
 Db 241 RVSVNTNFAARGDPSLRIDELEADEGIYSCHLHHYCHLHRRVPHLQVTEPAPEPPAR 300
 Qy 201 GSPGSSGSHGAPGPOPTLARGHNVINIVPESRAHFFQOLGYVLATLLLFILLITVLL 260
 Db 301 ASPGSGSHGSAFSPDPTLTRGHSINIVIPEDHTFFQOLGYVLATLLLFILLITVLL 360
 Qy 261 AARRRR-GGYEYSDKSGKSGKVDNLAFVAVAGDMLYRSEDILQDYKNILKERAE 319
 Db 361 ATRHSGGCKTSKAGSKGKVDNMVFAVATRDQAPYRTEDIQDYKNILKERAE 420
 Qy 320 AHSPLPAKYIDLKGRKENCK 341
 Db 421 AHSPLPAKVDLDKEFKEYCK 442

RESULT 10

ABBI0350
 ID ABB10350 standard; Protein; 269 AA.

XX AC ABB10350;

XX DT 10-JAN-2002 (first entry)

XX DE Human cDNA SEQ ID NO: 658.

XX KW Human; gene therapy; neural disorder; immune system disorder;
 XX muscular disorder; reproductive disorder; gastrointestinal disorder;
 XX pulmonary disorder; cardiovascular disorder; renal disorder;
 XX proliferative disorder; inflammation.

XX OS Homo sapiens.

XX FN W0200154474-A2.

XX PD 02-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US01349.

XX XX 31-JAN-2000; 2000US-17906SP.

XX PR 04-FEB-2000; 2000US-18062SP.

PR 24-FEB-2000; 2000US-184664P.
 PR 02-MAR-2000; 2000US-186350P.
 PR 16-MAR-2000; 2000US-189874P.
 PR 17-MAR-2000; 2000US-190076P.
 PR 18-APR-2000; 2000US-198123P.
 PR 19-MAY-2000; 2000US-205515P.
 PR 07-JUN-2000; 2000US-209467P.
 PR 28-JUN-2000; 2000US-215135P.
 PR 30-JUN-2000; 2000US-216647P.
 PR 07-JUL-2000; 2000US-216880P.
 PR 11-JUL-2000; 2000US-217487P.
 PR 11-JUL-2000; 2000US-217496P.
 PR 14-JUL-2000; 2000US-218290P.
 PR 26-JUL-2000; 2000US-220964P.
 PR 26-JUL-2000; 2000US-220964P.
 PR 14-AUG-2000; 2000US-224518P.
 PR 14-AUG-2000; 2000US-224519P.
 PR 14-AUG-2000; 2000US-225213P.
 PR 14-AUG-2000; 2000US-225214P.
 PR 14-AUG-2000; 2000US-225266P.
 PR 14-AUG-2000; 2000US-225267P.
 PR 14-AUG-2000; 2000US-225268P.
 PR 14-AUG-2000; 2000US-225270P.
 PR 14-AUG-2000; 2000US-225447P.
 PR 14-AUG-2000; 2000US-225757P.
 PR 14-AUG-2000; 2000US-225758P.
 PR 14-AUG-2000; 2000US-225759P.
 PR 18-AUG-2000; 2000US-226279P.
 PR 22-AUG-2000; 2000US-226681P.
 PR 22-AUG-2000; 2000US-226686P.
 PR 22-AUG-2000; 2000US-227182P.
 PR 23-AUG-2000; 2000US-227009P.
 PR 30-AUG-2000; 2000US-228924P.
 PR 01-SEP-2000; 2000US-229287P.
 PR 01-SEP-2000; 2000US-229343P.
 PR 01-SEP-2000; 2000US-229344P.
 PR 01-SEP-2000; 2000US-229345P.
 PR 05-SEP-2000; 2000US-229509P.
 PR 05-SEP-2000; 2000US-229513P.
 PR 06-SEP-2000; 2000US-230437P.
 PR 06-SEP-2000; 2000US-230438P.
 PR 08-SEP-2000; 2000US-231242P.
 PR 08-SEP-2000; 2000US-231243P.
 PR 08-SEP-2000; 2000US-231244P.
 PR 08-SEP-2000; 2000US-231413P.
 PR 08-SEP-2000; 2000US-231414P.
 PR 08-SEP-2000; 2000US-232080P.
 PR 08-SEP-2000; 2000US-232081P.
 PR 12-SEP-2000; 2000US-231968P.
 PR 14-SEP-2000; 2000US-232397P.
 PR 14-SEP-2000; 2000US-232398P.
 PR 14-SEP-2000; 2000US-232399P.
 PR 14-SEP-2000; 2000US-232400P.
 PR 14-SEP-2000; 2000US-232401P.
 PR 14-SEP-2000; 2000US-233063P.
 PR 14-SEP-2000; 2000US-233064P.
 PR 14-SEP-2000; 2000US-233065P.
 PR 21-SEP-2000; 2000US-234223P.
 PR 21-SEP-2000; 2000US-234274P.
 PR 25-SEP-2000; 2000US-234997P.
 PR 25-SEP-2000; 2000US-234998P.
 PR 26-SEP-2000; 2000US-235484P.
 PR 27-SEP-2000; 2000US-235834P.
 PR 27-SEP-2000; 2000US-235836P.
 PR 29-SEP-2000; 2000US-236327P.
 PR 29-SEP-2000; 2000US-236376P.
 PR 29-SEP-2000; 2000US-236368P.
 PR 29-SEP-2000; 2000US-236369P.
 PR 29-SEP-2000; 2000US-236370P.
 PR 02-OCT-2000; 2000US-236802P.
 PR 02-OCT-2000; 2000US-237037P.
 PR 02-OCT-2000; 2000US-237038P.

PR 02-OCT-2000; 2000US-237039P.
PR 02-OCT-2000; 2000US-237040P.
PR 13-OCT-2000; 2000US-239935P.
PR 13-OCT-2000; 2000US-239937P.
PR 20-OCT-2000; 2000US-240960P.
PR 20-OCT-2000; 2000US-241221P.
PR 20-OCT-2000; 2000US-241785P.
PR 20-OCT-2000; 2000US-241786P.
PR 20-OCT-2000; 2000US-241787P.
PR 20-OCT-2000; 2000US-241809P.
PR 20-OCT-2000; 2000US-241809P.
PR 20-OCT-2000; 2000US-241826P.
PR 01-NOV-2000; 2000US-244617P.
PR 08-NOV-2000; 2000US-246474P.
PR 08-NOV-2000; 2000US-246475P.
PR 08-NOV-2000; 2000US-246476P.
PR 08-NOV-2000; 2000US-246477P.
PR 08-NOV-2000; 2000US-246478P.
PR 08-NOV-2000; 2000US-246523P.
PR 08-NOV-2000; 2000US-246524P.
PR 08-NOV-2000; 2000US-246525P.
PR 08-NOV-2000; 2000US-246526P.
PR 08-NOV-2000; 2000US-246527P.
PR 08-NOV-2000; 2000US-246528P.
PR 08-NOV-2000; 2000US-246532P.
PR 08-NOV-2000; 2000US-246609P.
PR 08-NOV-2000; 2000US-246610P.
PR 08-NOV-2000; 2000US-246611P.
PR 08-NOV-2000; 2000US-246613P.
PR 17-NOV-2000; 2000US-249207P.
PR 17-NOV-2000; 2000US-249208P.
PR 17-NOV-2000; 2000US-249209P.
PR 17-NOV-2000; 2000US-249210P.
PR 17-NOV-2000; 2000US-249211P.
PR 17-NOV-2000; 2000US-249212P.
PR 17-NOV-2000; 2000US-249213P.
PR 17-NOV-2000; 2000US-249214P.
PR 17-NOV-2000; 2000US-249215P.
PR 17-NOV-2000; 2000US-249216P.
PR 17-NOV-2000; 2000US-249217P.
PR 17-NOV-2000; 2000US-249218P.
PR 17-NOV-2000; 2000US-249244P.
PR 17-NOV-2000; 2000US-249245P.
PR 17-NOV-2000; 2000US-249264P.
PR 17-NOV-2000; 2000US-249265P.
PR 17-NOV-2000; 2000US-249297P.
PR 17-NOV-2000; 2000US-249299P.
PR 01-DEC-2000; 2000US-250160P.
PR 01-DEC-2000; 2000US-250391P.
PR 05-DEC-2000; 2000US-251039P.
PR 05-DEC-2000; 2000US-251988P.
PR 06-DEC-2000; 2000US-256719P.
PR 06-DEC-2000; 2000US-251479P.
PR 08-DEC-2000; 2000US-251856P.
PR 08-DEC-2000; 2000US-251868P.
PR 08-DEC-2000; 2000US-251869P.
PR 08-DEC-2000; 2000US-251989P.
PR 08-DEC-2000; 2000US-251990P.
PR 11-DEC-2000; 2000US-254097P.
PR 05-JAN-2001; 2001US-259678P.

(HUMA-) HUMAN GENOME SCI INC.
PR Rosen CA, Barash SC, Ruben SM;
PR WPI; 2001-476161/51.
PR N-PSDB; ABA06572.
PT Isolated nucleic acid molecule encoding an inflammation-associated
PT polypeptide is used in preventing, treating or ameliorating a medical
PT condition -
XX

PS Claim 11; SEQ ID NO: 658; 859pp + Sequence Listing; English.
XX
CC The present invention provides human cDNAs, proteins and related genomic
CC DNAs. These can be used in the treatment of neural, immune system,
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC renal and proliferative disorders and inflammation. The present sequence
CC is a protein of the invention.
XX
SQ Sequence 269 AA;

Query Match 71.6%; Score 1300; DB 22; Length 269;
Best Local Similarity 98.4%; Pred. No. 9.8e-109;
Matches 239; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 40 HHYCHLYESLAVRLEVTDPATPAYWDGKEVLAVARGAPALLTCVNRGHVWTDHVEE 99
|||
Db 4 HHYCHLYESLAVRLEVTDPATPAYWDGKEVLAVARGAPALLTCVNRGHVWTDHVEE 63
|||

QY 100 AQQVVHWRQPPGVPHDRADRLDLYASGERRAYGPIFLDRVAVGADAFERGFSLRIE 159
|||
Db 64 AQQVVHWRQPPGVPHDRADRLDLYASGERRAYGPIFLDRVAVGADAFERGFSLRIE 123
|||

QY 160 PLEVADEGTYSCHLHHYCGLHERRVFLHTVAEPHAEPPPPGSGSGSGAGPDPPTL 219
|||
Db 124 PLEVADEGTYSCHLHHYCGLHERRVFLHTVAEPHAEPPPPGSGSGSGAGPDPPTL 183
|||

QY 220 ARGHNVINVIPEGRAHFFQOLGYVLATLLFILLVTVLLAARRRRGGYEYSQKSGKS 279
|||
Db 184 ARGHNVINVIPEGRAHFFQOLGYVLATLLFILLVTVLLAARRRRGGYEYSQKSGSQ 243
|||

QY 280 KGK 282
:
Db 244 RGR 246

RESULT 11
ABP66937
ID ABP66937 standard; Protein; 269 AA.
XX
AC ABP66937;
XX
DT 09-DEC-2002 (first entry)
XX
DE Human polypeptide SEQ ID NO 658.
XX
KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
KW antiparkinsonian; antiseizure; antianaemic; antiarthritic; cancer;
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine.
XX
OS Homo sapiens.
XX
PN US2002090672-A1.
XX
PD 11-JUL-2002.
XX
PF 17-JAN-2001; 2001US-0764853.
XX
PR 31-JAN-2000; 2000US-179065P.
PR 04-FEB-2000; 2000US-180628P.
PR 28-JUN-2000; 2000US-214886P.
PR 07-JUL-2000; 2000US-216647P.
PR 07-JUL-2000; 2000US-216880P.
PR 11-JUL-2000; 2000US-217487P.
PR 11-JUL-2000; 2000US-217496P.
PR 14-JUL-2000; 2000US-218290P.
PR 26-JUL-2000; 2000US-220963P.
PR 26-JUL-2000; 2000US-220964P.
PR 14-AUG-2000; 2000US-224518P.
PR 14-AUG-2000; 2000US-224519P.

PR 14-AUG-2000; 2000US-225267P.
PR 14-AUG-2000; 2000US-225268P.
PR 14-AUG-2000; 2000US-225270P.
PR 14-AUG-2000; 2000US-225447P.
PR 14-AUG-2000; 2000US-225757P.
PR 14-AUG-2000; 2000US-225758P.
PR 22-AUG-2000; 2000US-226868P.
PR 30-AUG-2000; 2000US-228924P.
PR 01-SEP-2000; 2000US-229287P.
PR 01-SEP-2000; 2000US-229343P.
PR 01-SEP-2000; 2000US-229344P.
PR 01-SEP-2000; 2000US-229345P.
PR 05-SEP-2000; 2000US-229509P.
PR 05-SEP-2000; 2000US-229513P.
PR 08-SEP-2000; 2000US-231413P.
PR 21-SEP-2000; 2000US-234223P.
PR 21-SEP-2000; 2000US-234274P.
PR 25-SEP-2000; 2000US-234997P.
PR 27-SEP-2000; 2000US-235834P.
PR 29-SEP-2000; 2000US-236327P.
PR 29-SEP-2000; 2000US-236367P.
PR 29-SEP-2000; 2000US-236368P.
PR 29-SEP-2000; 2000US-236369P.
PR 29-SEP-2000; 2000US-236370P.
PR 02-OCT-2000; 2000US-236802P.
PR 02-OCT-2000; 2000US-237037P.
PR 02-OCT-2000; 2000US-237038P.
PR 02-OCT-2000; 2000US-237039P.
PR 02-OCT-2000; 2000US-237040P.
PR 13-OCT-2000; 2000US-239935P.
PR 20-OCT-2000; 2000US-240960P.
PR 20-OCT-2000; 2000US-241785P.
PR 20-OCT-2000; 2000US-241809P.
PR 01-NOV-2000; 2000US-244817P.
PR 17-NOV-2000; 2000US-249299P.
PR 08-DEC-2000; 2000US-251856P.
PR 08-DEC-2000; 2000US-251868P.
PR 08-DEC-2000; 2000US-251869P.
XX (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
XX
PI Rosen CA, Ruben SM, Barash SC;
XX
XX WPI; 2002-681727/73.
XX N-PSDB; ABV83903.
XX
XX Novel polypeptide useful for diagnosis, prognosis, prevention, and
PT treatment of immune, hyperproliferative, renal, respiratory,
PT cardiovascular, reproductive, endocrine, gastrointestinal and
PT neurological disorders -
XX
XX Claim 11; SEQ ID NO 658; 369pp + Sequence Listing; English.
XX
XX The invention relates to novel genes (ABV83682-ABV84101) and proteins
CC (ABP66710-ABP67129) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 269 AA;
Query Match 71.6%; Score 1300; DB 23; Length 269;
Best Local Similarity 98.4%; Pred. No. 9.8e-109;
Matches 239; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 40 HHYCHLYESLAVRLEVTGGPPATPAYWDGKEVLAVAGAPALLTCVNKRHWTDHVEE 99
DB 4 HHYCHLYESLAVRLEVTGGPPATPAYWDGKEVLAVAGAPALLTCVNKRHWTDHVEE 63
QY 100 AQQVHWDRQPPGVPHDRADRLLDLYASGERRAYGFLRDRVAVGADAFERGFSLRIE 159
DB 64 AQQVHWDRQPPGVPHDRADRLLDLYASGERRAYGFLRDRVAVGADAFERGFSLRIE 123
QY 160 PLEVADEGTYSCHLHHYCGLHRRVFLTVAPHAEPPEPRGSPNGSSHGAPGPDPTL 219
DB 124 PLEVADEGTYSCHLHHYCGLHRRVFLTVAPHAEPPEPRGSPNGSSHGAPGPDPTL 183
QY 220 ARGHNVINIVPESRAHFFQQLGYVLATLLFILLVTVLLAARRRGGEYSDOKSGKS 279
DB 184 ARGHNVINIVPESRAHFFQQLGYVLATLLFILLVTVLLAARRRGGEYSDOKSGSQ 243
QY 280 KGK 282
DB 244 RGR 246
RESULT 12
AAB59011
ID AAB59011 standard; Protein; 290 AA.
XX AC AAB59011;
XX 27-MAR-2001 (first entry)
XX DE Breast and ovarian cancer associated antigen protein sequence SEQ ID 719.
XX KW Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
KW neotropic; neuroprotective; antiviral; antiallergic; hepatotropic;
KW antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant;
KW antibacterial; antifungal; antiparasitic; cardiant; immune disorder;
KW Addison's disease; allergy; autoimmune haemolytic anaemia;
KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
KW cardiovascular disorder; wound healing; neurological disease.
XX OS Homo sapiens.
XX WO200055173-A1.
XX PN 21-SEP-2000.
XX PD 08-MAR-2000; 2000WO-US05881.
XX PF 12-MAR-1999; 99US-0124270.
XX PR (HUMA-) HUMAN GENOME SCI INC.
XX PA Rosen CA, Ruben SM;
XX PI WPI; 2000-611515/58.
XX DR N-PSDB; AAF21914.
XX PT New human breast and ovarian cancer associated gene sequences and the
PT polypeptides encoded by these genes, useful in the prevention,
PT treatment and diagnosis of cancer, immune disorders, cardiovascular
PT disorders and neurological diseases -
XX PS Claim 11; Page 1173-1174; 1299pp; English.
XX Sequences AAF21614 - AAF22031 represent DNA sequences encoding human
CC proteins AAB58711 - AAB59128. The DNA and protein sequences are

CC associated with breast and ovarian cancer. Included in the invention are
CC sequences AAF2032 - AAF2040 and AAF59129 which are used in the
CC isolation and characterisation of the DNA and protein sequences of the
CC invention. The breast and ovarian cancer associated DNA, protein, agonist
CC or antagonist sequences exhibit cytostatic; immunosuppressive;
CC neutrotic; neuroprotective; antiviral; antiallergic; hepatotropic;
CC antidiabetic; antiinflammatory; antitumor; vulnary; anticonvulsant;
CC antibacterial; antifungal; antiparasitic and cardiac activity. The
CC polynucleotide and protein sequences are used in the diagnosis of cancer,
CC particularly breast and ovarian cancer. The nucleic acid sequences,
CC proteins, agonists and antagonists may also be used in the diagnosis,
CC prevention and treatment of immune disorders e.g. Addison's disease,
CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
CC arthritis and ulcerative colitis; cardiovascular disorders such as
CC myocardial ischaemias; wound healing; neurological diseases such as
CC cerebral anoxia and epilepsy; and infectious diseases.

XX Sequence 290 AA;

Query Match 55.4%; Score 1006; DB 21; Length 290;
Best Local Similarity 64.6%; Pred. No. 3.1e-82;
Matches 210; Conservative 8; Mismatches 55; Indels 52; Gaps 5;
QY 21 LLHSAVETDAGLYTCNLHHYCHLYESLAVRLEVTGDPATPAYWDGEKVLAVARGAP 80
Db 14 LLRAVEETDAGLYTCNLHHYCHLYESLAVRLEVTGDPATPAYWDGEKVLAVARGAP 72
QY 81 ALLTCVNRGHVWTDHVEEAQVWHDROPVPHDRADRLDLYASGERAYGFLRLD 140
Db 73 AXLTVCVNRGHVWTDHVEEAQVWHDROPVPHDRADRLDLYASGERAYGFLRLD 131
QY 141 RVAVGADAFERGFSLRIEPLVADGTYSCHLHHYCHLHERRVFLTVAEPAHPPPR 200
Db 132 RVAVGADAFERGFSLRIEPLVADGTYSCHLHHYCHLHERRVFLTVAEPAHPPPR 168
QY 201 GSPNGSSHGAPGPDPTLARGHNVINIVPESRAHF-----FQGLGVLTALLFILLV 256
Db 169 WRAATTSSMSSPRAEPTSSSWATCPRCCSSCYMSLSSWPPAG-----214
QY 257 TVLLAARRRGVYSDOKSGKGDVNLAEFAVAGDQMLYRSEDQLDYKNNILKER 316
Db 215 -----RGTEYSYDOKSGKGDVNLAEFAVAGDQMLYRSEDQLDYKNNILKER 265
QY 317 AELAHSPLPKAYIDLDGFRKENCK 341
Db 266 AELAHSPLPKAYIDLDGFRKENCK 290

RESULT 13

ABBI0523
ID ABB10523 standard; Protein; 192 AA.

AC ABB10523;

XX 10-JAN-2002 (first entry)

DT Human cDNA SEQ ID NO: 831.

DE XX

XX Human; gene therapy; neural disorder; immune system disorder;
KW muscular disorder; reproductive disorder; gastrointestinal disorder;
KW pulmonary disorder; cardiovascular disorder; renal disorder;
KW proliferative disorder; inflammation.

XX Homo sapiens.

OS WO200154474-A2.

FN 02-AUG-2001.

PD 17-JAN-2001; 2001WO-US01349.

PF 31-JAN-2000; 2000US-179065P.

XX 02-OCT-2000; 2000US-236802P.

FR 02-OCT-2000; 2000US-237037P.

PR 04-FEB-2000; 2000US-180628P.
PR 24-FEB-2000; 2000US-184664P.
PR 02-MAR-2000; 2000US-186350P.
PR 16-MAR-2000; 2000US-189874P.
PR 17-MAR-2000; 2000US-190076P.
PR 18-APR-2000; 2000US-198123P.
PR 19-MAY-2000; 2000US-205515P.
PR 07-JUN-2000; 2000US-203467P.
PR 28-JUN-2000; 2000US-214886P.
PR 30-JUN-2000; 2000US-215135P.
PR 07-JUL-2000; 2000US-216647P.
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PR 26-JUL-2000; 2000US-220963P.
PR 26-JUL-2000; 2000US-220964P.
PR 14-AUG-2000; 2000US-224518P.
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PR 14-AUG-2000; 2000US-225266P.
PR 14-AUG-2000; 2000US-225268P.
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PR 22-AUG-2000; 2000US-227182P.
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PR 01-SEP-2000; 2000US-229287P.
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PR 05-SEP-2000; 2000US-229509P.
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PR 08-SEP-2000; 2000US-231414P.
PR 08-SEP-2000; 2000US-232080P.
PR 08-SEP-2000; 2000US-232081P.
PR 12-SEP-2000; 2000US-231968P.
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PR 14-SEP-2000; 2000US-233063P.
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PR 21-SEP-2000; 2000US-234223P.
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20-OCT-2000; 2000US-241787P.
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01-NOV-2000; 2000US-244617P.
08-NOV-2000; 2000US-246474P.
08-NOV-2000; 2000US-246475P.
08-NOV-2000; 2000US-246476P.
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08-NOV-2000; 2000US-246532P.
08-NOV-2000; 2000US-246609P.
08-NOV-2000; 2000US-246610P.
08-NOV-2000; 2000US-246611P.
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17-NOV-2000; 2000US-249216P.
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17-NOV-2000; 2000US-249245P.
17-NOV-2000; 2000US-249264P.
17-NOV-2000; 2000US-249265P.
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01-DEC-2000; 2000US-250160P.
01-DEC-2000; 2000US-250391P.
05-DEC-2000; 2000US-251030P.
05-DEC-2000; 2000US-251988P.
05-DEC-2000; 2000US-256719P.
06-DEC-2000; 2000US-251479P.
08-DEC-2000; 2000US-251856P.
08-DEC-2000; 2000US-251868P.
08-DEC-2000; 2000US-251869P.
08-DEC-2000; 2000US-251989P.
08-DEC-2000; 2000US-251990P.
11-DEC-2000; 2000US-254097P.
05-JAN-2001; 2001US-259678P.
(HUMA-) HUMAN GENOME SCI INC.
Rosen CA, Barash SC, Ruben SM;
WPI; 2001-476161/51.
N-PSDB; ABA06745.
Isolated nucleic acid molecule encoding an inflammation-associated polypeptide is used in preventing, treating or ameliorating a medical condition

XX Claim 11; SEQ ID NO: 831; 859pp + Sequence Listing; English.
PS The present invention provides human cDNAs, proteins and related genomic
XX DNAs. These can be used in the treatment of neural, immune system,
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC renal and proliferative disorders and inflammation. The present sequence
CC is a protein of the invention.
XX
SQ Sequence 192 AA;
Query Match 52.6%; Score 955; DB 22; Length 192;
Best Local Similarity 98.9%; Pred. No. 7.2e-78;
Matches 174; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 21 LLHSAVEETDAGLYTCNLHHYCHLYESLAVRLEVTGPPATPAYWDGKEVLAVARGAP 80
Db 17 LLIRAVEETDAGLYTCNLHHYCHLYESLAVRLEVTGPPATPAYWDGKEVLAVARGAP 76
QY 81 ALLTCVNRGHVWTDRLHVEEAQQVHWDROPVGVPHDRADRLDLVSGERRAYGFLFLRD 140
Db 77 ALLTCVNRGHVWTDRLHVEEAQQVHWDROPVGVPHDRADRLDLVSGERRAYGFLFLRD 136
QY 141 RVAVGADAFERGFSLRIEPLVADGTYSCLLHHYCGLHERRVHLLTVAEPHAE 196
Db 137 RVAVGADAFERGFSLRIEPLVADGTYSCLLHHYCGLHERRVHLLTVAEPHAE 192
RESULT 14
AAU18028
ID AAU18028 standard; Protein; 192 AA.
XX AAU18028;
DT 07-NOV-2001 (first entry)
DE Human immunoglobulin polypeptide SEQ ID No 173.
XX Immunoglobulin; signal transduction pathway protein; cancer;
KW antitense therapy; gene therapy; neurological disorder; renal disorder;
KW cardiovascular disorder; gastrointestinal disorder; pulmonary disorder;
KW reproductive disorder; immune system disorder; proliferative disorder;
KW muscular disorder.
XX Homo sapiens.
XX WO200155315-A2.
XX 02-AUG-2001.
XX 17-JAN-2001; 2001WO-US01326.
XX 31-JAN-2000; 2000US-0179065.
XX 04-FEB-2000; 2000US-0180628.
XX 24-FEB-2000; 2000US-0184664.
XX 02-MAR-2000; 2000US-0186350.
XX 16-MAR-2000; 2000US-0189874.
XX 17-MAR-2000; 2000US-0190076.
XX 18-APR-2000; 2000US-0198123.
XX 19-MAY-2000; 2000US-0205515.
XX 07-JUN-2000; 2000US-0209467.
XX 28-JUN-2000; 2000US-0214886.
XX 30-JUN-2000; 2000US-0215135.
XX 07-JUL-2000; 2000US-0216647.
XX 07-JUL-2000; 2000US-0216880.
XX 11-JUL-2000; 2000US-0217487.
XX 11-JUL-2000; 2000US-0217496.
XX 14-JUL-2000; 2000US-0218290.
XX 26-JUL-2000; 2000US-0220963.
XX 26-JUL-2000; 2000US-0220964.
XX 14-AUG-2000; 2000US-0224518.
XX 14-AUG-2000; 2000US-0224519.
XX 14-AUG-2000; 2000US-0225213.

PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225457.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
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PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
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PR 06-SEP-2000; 2000US-0230437.
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PR 08-SEP-2000; 2000US-0231242.
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PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
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PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234597.
PR 25-SEP-2000; 2000US-0234598.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239335.
PR 13-OCT-2000; 2000US-0239337.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 01-NOV-2000; 2000US-0244617.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.

PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
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PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
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PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-457725/49.
XX N-PSDB; AAS28816.
XX Isolated novel immunoglobulin polypeptide for monitoring the presence.
XX and progression of diseases and for diagnosis -
XX Claim 11; SEQ ID No 173; 551pp; English.
XX Sequences AAU17977-AAU18087 represent immunoglobulin polypeptides of the
XX invention. The polypeptides and their associated polynucleotides can be
XX used to diagnose a pathological condition or a susceptibility to a
XX pathological condition in a subject by determining the presence or
XX absence of a mutation in a DNA sequence or determining the presence or
XX amount of expression of the protein. Alternatively the identification of
XX a binding partner to a sequence allows determination of changes in
XX protein activity. The sequences can be used as research tools for
XX receptors or other signal transduction pathway proteins that interact
XX with the polypeptides of the invention and can be used to treat, prevent
XX or diagnose various types of disorders such as neurological disorders,
XX cardiovascular disorders, gastrointestinal disorders, reproductive
XX disorders, immune system disorders, renal disorders, muscular disorders,
XX pulmonary disorders, proliferative disorders and cancer.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.

	Query Match	52.6%	Score 955	DB 23	Length 192
	Best Local Similarity	98.9%	Prod. No. 7.2e-79		
	Matches 174	Conservative 0	Mismatches 2	Indels 0	Gaps 0
21	LLHSAVETDAGLTYCNLHHYCHLYESLAVRLEVTGPPATPAYDGEKEVLAVAGAP	80			
17	LLIRAVETDAGLTYCNLHHYCHLYESLAVRLEVTGPPATPAYDGEKEVLAVAGAP	76			
81	ALLTCVNRGHVWTDHRVVEAAQCVVHWDQPPGVPHDRADRLDLLYASGERRAYGFLFURD	140			
77	ALLTCVNRGHVWTDHRVVEAAQCVVHWDQPPGVPHDRADRLDLLYASGERRAYGFLFURD	136			
141	RVAVGADAFERGDPSLRLEPVEADGTYSCHLHHYHCGLHERRRVFHLTVAPHPAE	196			

Db 137 RVAVGADAFERGFSLRIPPLEVADEGTYSCHLHHHYCGLHRRVPHLTVAEPHAE 192

Search completed: February 13, 2004, 15:30:19
Job time : 46 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2004, 15:30:22 ; Search time 41 Seconds
(without alignments)
2146.242 Million cell updates/sec

Title: US-10-006-818A-77

Perfect score: 1816

Sequence: 1 MALPSRILLKWLQSSAV.....SPLPAKYIDLKGRKENCK 341

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriopl:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1755.5	96.7	442	Q9BRK3	Q9brk3 homo sapien
2	1694.5	93.3	450	Q96K3	Q96kc3 homo sapien
3	1362.5	75.0	442	Q920S7	Q920s7 mus musculus
4	1358.5	74.8	442	Q9DBV4	Q9dbv4 mus musculus
5	1079.5	59.4	437	Q90W14	Q90w14 gallus gall
6	129	7.1	686	Q9ERS6	Q9ers6 mus musculus
7	126	6.9	447	Q8NHJ6	Q8nhj6 homo sapien
8	123	6.8	650	Q8NHL6	Q8nhl6 homo sapien
9	123	6.8	650	Q75024	Q75024 homo sapien
10	122.5	6.7	651	Q8NHJ9	Q8nhj9 homo sapien
11	122	6.7	652	Q75025	Q75025 homo sapien
12	120.5	6.6	448	Q8NLC7	Q8nlc7 homo sapien
13	119.5	6.6	448	Q8NHL5	Q8nhl5 homo sapien
14	119.5	6.6	651	Q8NHK0	Q8nhk0 homo sapien
15	118.5	6.5	448	O15468	O15468 homo sapien
16	118.5	6.5	448	Q75021	Q75021 homo sapien

17	115.5	6.4	533	4	Q8NCB6	Q8ncb6 homo sapien
18	115.5	6.4	534	4	Q8NB18	Q8nb18 homo sapien
19	114	6.3	658	4	Q9NZN0	Q9nzn0 homo sapien
20	114	6.3	686	4	Q9NP60	Q9np60 homo sapien
21	113	6.2	1746	4	Q8WY19	Q8wy19 homo sapien
22	112	6.2	2013	11	Q8VHZ8	Q8vzh8 rattus norv
23	112	6.2	2013	11	Q9ERC8	Q9erc8 mus musculu
24	111.5	6.1	915	11	Q8R4B3	Q8r4b3 mus musculu
25	111.5	6.1	1723	11	Q8CHB2	Q8chb2 mus musculu
26	110.5	6.1	645	6	Q8MJZ5	Q8mjb5 pan troglod
27	110	6.1	597	4	Q8NHJ8	Q8nhj8 homo sapien
28	109.5	6.0	1044	4	Q96IW3	Q96iw3 homo sapien
29	109	6.0	1214	4	Q75054	Q75054 homo sapien
30	108.5	6.0	1214	4	O18906	O18906 macaca mula
31	108	5.9	381	4	Q9Y4A4	Q9y4a4 homo sapien
32	107.5	5.9	344	4	Q9UKV4	Q9ukv4 homo sapien
33	107.5	5.9	802	13	O42127	O42127 xenopus lae
34	107.5	5.9	1217	11	P97685	P97685 rattus norv
35	107.5	5.9	1842	4	Q8IZY3	Q8izy3 homo sapien
36	107.5	5.9	2053	4	Q8WU7	Q8wxu7 homo sapien
37	107.5	5.9	2053	4	Q8IZY4	Q8izy4 homo sapien
38	107.5	5.9	2113	4	Q8TD84	Q8td84 homo sapien
39	106.5	5.9	183	4	Q9UEL6	Q9uel6 homo sapien
40	106.5	5.9	1041	4	Q94856	Q94856 homo sapien
41	106	5.8	209	4	Q9NYK4	Q9nyk4 homo sapien
42	105.5	5.8	243	4	Q9UEL4	Q9uel4 homo sapien
43	105.5	5.8	598	4	Q8NHJ7	Q8nhj7 homo sapien
44	105.5	5.8	598	4	Q8N423	Q8n423 homo sapien
45	105.5	5.8	598	4	O75017	O75017 homo sapien

ALIGNMENTS

RESULT 1

Q9BRK3 PRELIMINARY; PRT; 442 AA.

AC Q9BRK3;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas, and Eye;
RA Strausberg R.;

RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006213; AAH06213.1; -.
DR EMBL; BC017312; AAH17312.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
SQ Hypothetical protein.

Q9 BRK3 442 AA; 49131 MW; B08F89D726222CA1 CRC64;
Query Match 96.7%; Score 1755.5; DB 4; Length 442;
Best Local Similarity 77.1%; Pred. No. 3.3e-157;
Matches 341; Conservative 0; Mismatches 0; Indels 101; Gaps 1;
SQ SEQUENCE 442 AA; 49131 MW; B08F89D726222CA1 CRC64;

QY 1 MALPSRILLKWLQSSAVLLHS----- 24

Db 1 MALPSRILLKWLQSSAVLLHS----- 60

QY 25 ----- 24

Db 61 WTQRLHQRVLEWLDLPGGGPARELLDLYSAGEQRYVEARDRGRLELSASAFDDGNF 120

QY 25 -----AVEETDAGLYTCNLHHYCHLYESLAVRLEVTGPPATPAYWDGKEKYLAVARGA 79
 DB 121 SLLIRAVEETDAGLYTCNLHHYCHLYESLAVRLEVTGPPATPAYWDGKEKYLAVARGA 180
 QY 80 PALLTCVNRGHVWTDHRYVEEAQQVHVWDRQPPGVPHDRADRLDLLYASGERRAYGPLEFLR 139
 DB 181 PALLTCVNRGHVWTDHRYVEEAQQVHVWDRQPPGVPHDRADRLDLLYASGERRAYGPLEFLR 240
 QY 140 DRVAVGADAFERGFSLRIEPLVADEGTYSCHLHHYCGLHERRVPHLTVAEPHAEPPPP 199
 DB 241 DRVAVGADAFERGFSLRIEPLVADEGTYSCHLHHYCGLHERRVPHLTVAEPHAEPPPP 300
 QY 140 DRVAVGADAFERGFSLRIEPLVADEGTYSCHLHHYCGLHERRVPHLTVAEPHAEPPPP 199
 DB 241 DRVAVGADAFERGFSLRIEPLVADEGTYSCHLHHYCGLHERRVPHLTVAEPHAEPPPP 300
 QY 200 RGSPPGSSSHSGAGPDPPTLARGHNVINIVPESRAHFFFOOLGYVLATLLFILLVTVL 259
 DB 301 RGSPPGSSSHSGAGPDPPTLARGHNVINIVPESRAHFFFOOLGYVLATLLFILLVTVL 360
 QY 260 LAARRRRGGYYSQKSGSKGKDVNLAEFAVAAGDQMLYRSEDIQLDYKNILKERAEL 319
 DB 361 LAARRRRGGYYSQKSGSKGKDVNLAEFAVAAGDQMLYRSEDIQLDYKNILKERAEL 420
 QY 320 AHSPLPAKYIDLKGRKCNCK 341
 DB 421 AHSPLPAKYIDLKGRKCNCK 442

RESULT 2

Q96KC3 ID Q96KC3 PRELIMINARY; PRT; 450 AA.
 AC Q96KC3;
 DT 01-DEC-2001 (TremBLrel. 19, Created)
 DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
 DE Hypothetical protein FLJ14363.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
 RA Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
 RA Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
 RA Wakamatsu A., Nakamura Y., Nagahara K., Masuho Y., Oshima A.;
 RT "NEO human cDNA sequencing project";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK027269; BAB55010.1; -;
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00047; IG; 2.
 DR SMART; SM00409; IG; 2.
 DR PROSITE; PS50835; IG_LIKE; 2.
 KW Hypothetical protein.
 SQ SEQUENCE 450 AA; 49606 MW; 52565CBB68B534A6 CRC64;

Query Match 93.3%; Score 1694.5; DB 4; Length 450;
 Best Local Similarity 75.5%; Pred. NO. 2e-151;
 Matches 332; Conservative 1; Mismatches 0; Indels 107; Gaps 2;
 QY 1 MALPSRILLKVLVLIQSSAVLIHS----- 24
 DB 1 MALPSRILLKVLVLIQSSAVLIHS----- 60
 QY 25 ----- 24
 DB 61 WTQDRLHQRVRLHWRDLPGRGPGPARLLDLYSAGEQRVYEARDGRLELSASAFDDGNF 120
 QY 25 -----AVEETDAGLYTCNLHHYCHLYESLAVRLEVTGPPATPAYWDGKEKYLAVARGA 79
 DB 121 SLLIRAVEETDAGLYTCNLHHYCHLYESLAVRLEVTGPPATPAYWDGKEKYLAVARGA 180

QY 80 PALLTCVNRGHVWTDHRYVEEAQQVHVWDRQPPGVPHDRADRLDLLYASGERRAYGPLEFLR 139
 DB 181 PALLTCVNRGHVWTDHRYVEEAQQVHVWDRQPPGVPHDRADRLDLLYASGERRAYGPLEFLR 240
 QY 140 DRVAVGADAFERGFSLRIEPLVADEGTYSCHLHHYCGLHERRVPHLTVAEPHAEPPPP 199
 DB 241 DRVAVGADAFERGFSLRIEPLVADEGTYSCHLHHYCGLHERRVPHLTVAEPHAEPPPP 300
 QY 200 RGSPPGSSSHSGAGPDPPTLARGHNVINIVPESRAHFFFOOLGYVLATLLFILLVTVL 259
 DB 301 RGSPPGSSSHSGAGPDPPTLARGHNVINIVPESRAHFFFOOLGYVLATLLFILLVTVL 360
 QY 260 LAARRRRGGYYSQKSGSKGKDVNLAEFAVAAGDQMLYRSEDIQLDYKNIL 313
 DB 361 LAARRRRGGYYSQKSGSKGKDVNLAEFAVAAGDQMLYRSEDIQLDYKNIL 420
 QY 314 KERAELAHSPPLPAKYIDLK 333
 DB 421 KERAELAHSPPLPAKYIDLK 440
 RESULT 3
 Q920S7 ID Q920S7 PRELIMINARY; PRT; 442 AA.
 AC Q920S7;
 DT 01-DEC-2001 (TremBLrel. 19, Created)
 DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
 DE Adipocyte-specific protein 3 (RIKEN CDNA 1200013A08 gene).
 GN 1200013A08RIK OR ASP3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tsuruga H.;
 RT "Adipocyte-specific protein 3, a novel protein upregulated during
 RT adipocyte differentiation.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; ABC040488; BAB68501.1; -;
 DR EMBL; BC026438; AAH26438.1; -;
 DR MGD; MGI:1922011; 1200013A08RIK.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00047; IG; 2.
 DR SMART; SM00409; IG; 2.
 DR PROSITE; PS50835; IG_LIKE; 2.
 SQ SEQUENCE 442 AA; 49765 MW; B129028EDB1B1844 CRC64;

Query Match 75.0%; Score 1362.5; DB 11; Length 442;
 Best Local Similarity 61.3%; Pred. NO. 4.5e-120;
 Matches 271; Conservative 21; Mismatches 49; Indels 101; Gaps 3;
 QY 1 MALPSRILLKVLVLIQSSAVLIHS----- 21
 DB 1 MELLSRVLLWKLLVLIQSSAVLIHS----- 60
 QY 22 ----LHS----- 24
 DB 61 TQDRLHQRVRLHWRDLPGRGPGPARLLDLYSAGEQRVYEARDGRLELSASAFDDGNF 120
 QY 25 -----AVEETDAGLYTCNLHHYCHLYESLAVRLEVTGPPATPAYWDGKEKYLAVARGA 80
 DB 121 LLIRAVEERDAGLYTCNLHHYCHLYESLAVRLEVTGPPATPAYWDGKEKYLAVARGA 180

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QY 81 ALLTCVNRGHVWTDHRVBERAQVWVHWDROPVGVPHDRADRLDLVYASGERRAYGFLFLRD 140
Db 181 ALMTCINRAHVWTDRELEEAQVWVHWDROLPGVSHDRADRLDLVYASGERRAYGFLFLRD 240
QY 141 RVAGADAFERGFSLRISPLEVADEGTYSCHLHHYCGLHERRVFLHVAEPHAEPPPR 200
Db 241 RVSVNTNARAGDFSLRIDELEADSGIYCHLHHYCGLHERRVFLHVAEPHAEPPAR 300
QY 201 GSPGNGSSHGAPGPDPTLARGHNVINIVPESRAHFFQOLGVYLAATLLFILLVTVLL 260
Db 301 ASPGNGSGHSSAPSPDPTLTRGHSIINVIVPEDHTHFFQOLGVYLAATLLFILLVTVL 360
QY 261 AARRRR-GGVEYDQSGKSGKDVNLAEPFAVAGDQMLYRSEDIDQDYKNNILKERAE 319
Db 361 ATRHRSGGCKTSDKAGKSGKDVNMVZFNAVTRDQAPRYRDIQDYKNNILKERAE 420
QY 320 AHSPLPAKYIDLDKGRKENCK 341
Db 421 AHSPLPAKVDLDKFRKEYCK 442

RESULT 4
Q9DBV4 PRELIMINARY; PRT; 442 AA.
AC Q9DBV4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE 1200013A08RIK protein.
GN 1200013A08RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Giesi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamly M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.,
RI Functional annotation of a full-length mouse cDNA collection.;
RL Nature 409:685-690(2001).
DR EMBL; AK004732; BAB23514.1; -
DR MGD; MGI:1922011; 1200013A08RIK.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG LIKE; 2.
SQ SEQUENCE 442 AA; 49750 MW; 9600816B14AAAEF CRC64;

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Query Match 74.8%; Score 1358.5; DB 13; Length 442;
Best Local Similarity 61.1%; Pred. No. 1.1e-119;
Matches 270; Conservative 22; Mismatches 49; Indels 101; Gaps 3;
QY 1 MALPSRILLWKLVLLQSSAVL-----21

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Db 1 MELLUSRVLLWKLVLLQSSAVLSGPGSCTAAASSLVSESVSVAAGTQAVLRCSQSPRMVW 60
QY 22 ----LHS-----24
Db 61 TQDLRHDRQRVVHMDLGGPGSQRRRLVDMYSAGEQQRVVEPRDRDRLLSPSAFHDGNS 120
QY 25 ----AVETDAGLTGNLHHYCHLYESLAVRLEVTDGPPATPAYWDGEKEVLAVARGAP 80
Db 121 LLIRAVDRGEGVYTCNLHHYCHLDES LVRLEVTDPLLSRAYWDGEKEVLVAARGAP 180
QY 81 ALLTCVNRGHVWTDHRVBERAQVWVHWDROPVGVPHDRADRLDLVYASGERRAYGFLFLRD 140
Db 181 ALMTCINRAHVWTDRELEEAQVWVHWDROLPGVSHDRADRLDLVYASGERRAYGFLFLRD 240
QY 141 RVAGADAFERGFSLRISPLEVADEGTYSCHLHHYCGLHERRVFLHVAEPHAEPPPR 200
Db 241 RVSVNTNARAGDFSLRIDELEADSGIYCHLHHYCGLHERRVFLHVAEPHAEPPAR 300
QY 201 GSPGNGSSHGAPGPDPTLARGHNVINIVPESRAHFFQOLGVYLAATLLFILLVTVLL 260
Db 301 ASPGNGSGHSSAPSPDPTLTRGHSIINVIVPEDHTHFFQOLGVYLAATLLFILLVTVL 360
QY 261 AAR-RRRGVEYDQSGKSGKDVNLAEPFAVAGDQMLYRSEDIDQDYKNNILKERAE 319
Db 361 ATRYHSGGCKTSDKAGKSGKDVNMVZFNAVTRDQAPRYRDIQDYKNNILKERAE 420
QY 320 AHSPLPAKYIDLDKGRKENCK 341
Db 421 AHSPLPAKVDLDKFRKEYCK 442

RESULT 5
Q90WI4 PRELIMINARY; PRT; 437 AA.
AC Q90WI4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Plasma membrane protein 1B3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Dong S., Halfter W.;
RT "An anti cell adhesive protein from embryonic chick kidney.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF373843; AAK55399.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG LIKE; 2.
SQ SEQUENCE 437 AA; 50703 MW; 398CC264A88D4711 CRC64;

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Query Match 59.4%; Score 1079.5; DB 13; Length 437;
Best Local Similarity 61.1%; Pred. No. 2.4e-93;
Matches 206; Conservative 43; Mismatches 79; Indels 9; Gaps 4;
QY 6 RILLWKLVLLQSSAVLLHSAVEETDAGLYTCNLHHYCHLYESLAVRLEVTDGPPATPAY 65
Db 109 RILMPQNAFTGNSFLVTKDVAESDAGVYCNLHHYCHLYETVKIQIDITKKAKAEY 168
QY 66 WDGEKEVLAVARGAPALLTCVNRGHVWTDRELEEAQVWVHWDROPVGVPHDRADRLDL 125
Db 169 WDGEKAVIVALEGSNVWLPVCVNRNHIWTERHSESEQQVWVHWDROPVGVPHDRADRL 228
QY 126 ASGERRAYGFLFLDRVAVAGADAFERGFSLRISPLEVADEGTYSCHLHHYCGLHERRV 185

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Db	229	ASGERSYGPLFIQKXNITDTAFALGDFSLRISELENADGTYSCHLHHYCGLHERRI	288
Qy	186	FHLTVAEHAHPPPRSGSPNGSSHGAPGDPPTLARGHNVINIVPESRAHFFQQLGYVL	245
Db	289	YQVFTEPVREK---KVNLTHTNTAPADPNVVRGHNVINIIPESRIHFFQQLGYVL	344
Qy	246	ATLLFILLVTVLAAARRR-GGYEYSDQKSGKGVNLAEPFAVAGDQMLYRSEDI	304
Db	345	ATLLFVLLIIVTPIETKRQGRGYEVNKKYGE--KOVNLEFTVDTTDLTQYKSEDI	401
Qy	305	QLDYKNNILKGEALAHSPAKYDILDLKGFPRKENCK	341
Db	402	RLDYKNNILKEAKEAQRS-FFAKNIDLKDFRKEYCK	437
RESULT 6			
Q9ERS6 PRELIMINARY; PRT; 686 AA.			
ID	Q9ERS6		
AC	Q9ERS6		
DT	01-MAR-2001	(TrEMBLrel. 16, Created)	
DT	01-MAR-2001	(TrEMBLrel. 16, Last sequence update)	
DT	01-MAR-2003	(TrEMBLrel. 23, Last annotation update)	
DE	TIGR1R-1.		
GN	ILIRAPL2.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
NCBI_TaxId	10090;		
NP	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE-20459050; PubMed-10882729;		
RA	Born T.E.; Smith D.E.; Garka K.E.; Renshaw B.R.; Bertles J.S.;		
RA	Sims J.E.;		
RT	"Identification and characterization of two members of a novel class		
RT	of the interleukin-1 receptor (IL-1R) family. Delineation of a new		
RT	class of IL-1R-related proteins based on signaling.";		
RL	J. Biol. Chem. 275:29946-29954(2000).		
DR	EMBL; AF284437; AAC23371.1; -.		
DR	MGD; MGI:1913106; Ilirapl2.		
DR	InterPro; IPR003599; IG.		
DR	InterPro; IPR007110; IG-like.		
DR	InterPro; IPR003006; IG_MHC.		
DR	InterPro; IPR004075; IL1_receptor1.		
DR	InterPro; IPR004077; IL1_receptor1p.		
DR	InterPro; IPR000157; TIR_domain.		
DR	Pfam; PF00047; IG; 3.		
DR	Pfam; PF01582; TIR; 1.		
DR	PRINTS; PR01539; INTRLEUKINR2.		
DR	PRINTS; PR01537; INTRLEUKINR1F.		
DR	SMART; SMC0409; IG; 2.		
DR	SMART; SMC0255; TIR; 1.		
DR	PROSITE; PSS0835; IG_LIKE; 3.		
DR	PROSITE; PSS0104; TIR; 1.		
DR	SEQUENCE 686 AA; 78797 MW; 36160D1CD5EB98264 CRC64;		

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Db      337          :|::||:-----VLLRKKDLIYKI-----355
QY     237 FFQQGGVLTATLILLFILLVT-----VLLAARRRRGGEYSDD 273
       : |::|||:
Db     356 --ELAGGLGAIFILLILLVVVKYNIELMLFYRFQGDETTD 397
           ::||:|:

RESULT 7
QBHLJ6 PRELIMINARY; PRT; 447 AA.
ID QBHJ6 AC
DT 01-OCT-2002 (TEMBRel. 22, Created)
DR 01-OCT-2002 (TEMBRel. 22, Last sequence update)
DE 01-MAR-2003 (TEMBRel. 23, Last annotation update)
DN Leukocyte immunoglobulin-like receptor-5.
GN LILRB5
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Canavez F.C.; Submitted (JUL-2000) to the EMBL/GenBank/DDJB databases.
RL ENBL; AP283988; AAL36992.1; -
DR InterPro; IPR003006; IG_MHC.
DS Pfam; PF00047; Ig_2.
KW Receptor.
SQ SEQUENCE 447 AA; 49193 MW; 6B1E83E2BB107814 CRC64;

Query Match 6.9%; Score 126; DB 4; Length 447;
Best Local Similarity 23.4%; Pred. No. 0.0031;
Matches 92; Conservative 35; Mismatches 134; Indels 132; Gaps 21;

QY    48 SLAVLRLEVDGPATPAYWDGKEVLAVARGAPALLTCVNRGHVW-----TDRHVEEA 100
       ||:||||:|::|:
Db   14 SLGFRTHMQAGLPKPTLWAEPGSVISWG-----NSVTWCQGTLEARAYRIDKE 63
       ||:||||:|::|:
QY   101 QQVHHWRDPFGVPFHORA----DLILDLYASGERRAY-----GPLFLRDVRVAVG 145
       ||:||||:|::|:
Db   64 ESPAPNDRQNPLEPKNKAREPISMTEDYA-GRYCYRYSPGVGWSPSPLDEL---VMTG 119
       ||:||||:|::|:
QY   146 A-----DAF-----ERGDPSL-----156
Db   120 AYSKPTLSALPSLVTSKGKVTLCCQRSPMDFTLLIKERAAPHLLHRSEHGAAQHQAEE 179
       ||:||||:~::~|:
QY   157 RIEPLEVADEGYSTCHLHH--HYCGLHERRVPHLTVAEPHAPEPPRPGSGNGSSHSIGA 212
       ||:||||:~::~|:
Db   180 FPMSPVTVSHGGTYRCFSHGHSHYLSSHPSDPLEIVSGSLSDERP--SPTRSVSTAAG 237
       ||:||||:~::~|:
QY   213 PGPDPTLARHNVINVIKPES--RAHFQQLGGVLTATLLLFI LLVTVL-----L 260
       ||:||||:~::~|:
Db   238 PEQPPLMPTS-----VPHSGLRHHEVIIIGVLWSILLSLLLFILLQHWROGKHRTL 291
       ||:||||:~::~|:
QY   261 AAR-----RRRGGEYSQDKSG-----KSCKGKNLAFAFAVA-----GDOMLYRS--- 301
       ||:||||:~::~|:
Db   292 AQROADFCRPFEGAEEPDKGLQRRSPAADVQGENFCAAKTKNTPEDGVEMDTRSPHD 351
       ||:||||:~::~|:
QY   302 EDIQ-LDY-KNNILKERAEIAAH--SPIPAKYID 330
       ||:||||:~::~|:
Db   352 EDPQAVTYAKYGHSRPREMASPPPSPLSGFEFLD 384
       ||:||||:~::~|:


RESULT 8
QBHLJ6 PRELIMINARY; PRT; 650 AA.
ID QBNHL6 AC
DT 01-OCT-2002 (TEMBRel. 22, Created)
DR 01-OCT-2002 (TEMBRel. 22, Last sequence update)
DE 01-MAR-2003 (TEMBRel. 23, Last annotation update)
DN Leukocyte immunoglobulin-like receptor 1.
GN LIR1.
```

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20395285; PubMed=10941837;
RX Liu W.R., Kim J., Nwankwo C., Ashworth L.K., Arm J.P.;
RT "Genomic organization of the human leukocyte immunoglobulin-like
RT receptors within the leukocyte receptor complex on chromosome
RT 19q13.4";
RL Immunogenetics 51:659-669(2000).
DR EMBL: AF189277; AAC08984.1; -.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003598; IG_c2.
DR Pfam: PF00047; IG_3.
DR SMART: SM00408; IGC2; 3.
DR PROSITE: PS00835; IG_LIKE; 2.
KW Immunoglobulin domain; Receptor.
SQ SEQUENCE 650 AA; 70819 MW; 549196EAED2767C CRC64;

Query Match      6.8%; Score 123; DB 4; Length 650;
Best Local Similarity 20.6%; Pred. No. 0.0098;
Matches 68; Conservative 39; Mismatches 105; Indels 118; Gaps 12;

QY 51 VRLEVTGPPATPAYWDGEKEVLAVARGAPALLTCVNRGHVWTDHVEEAQQVHWDROP 110
DB 326 VLSVQPGP-----TVASGENVTLCCSQGMQFTLTKEGAADPW----- 367
QY 111 PGVPHDRADRLDLVYASGERAYGFLRDRVAVGADAFERGFSLRIEPLVEADEGTY 170
DB 368 -----RLRSTYQSQKYQAEFFM-----GPTVSAHAGTYR 396
QY 171 CH---LHHYCGLHERRVFLHTVAEPHAEPPRPGSGNGSHSGAGPDPTLARGHNVIN 227
DB 397 CYGSSQSKPYLLTHPSDPLELVSGSGGP---SSPTTGTSTSGPEDQLPTGSD--- 450
QY 228 VIVPES--RAHFFQQLGYVLTALLFILLVTLAARRRGYGYEYSDQSGKSGKDVN 285
DB 451 ---PQSGLGRHLGVIGILVAVILLLLLLFLLRHRQGHWTSTQRK----- 498
QY 286 LAEFAVAAG-----DQMLYRS-----EDIQLDYKN----- 310
DB 499 -ADFQHPAGAVGPEPTDRGLQWRSSPAADAQENLYAAVKHTQPEDGVEMDTRSPHDEDP 557
QY 311 -----NILKERAELAH--SPLPAKYID 330
DB 558 QAVTYAEVKHSRPRREMASPPSLSGEFLD 587

RESULT 9
O75024 PRELIMINARY; PRT; 650 AA.
AC O75024;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE Leucocyte immunoglobulin-like receptor-1 (leukocyte immunoglobulin-
DE like receptor, subfamily B (with TM and ITIM domains), member 1).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Cosman D., Fanger N., Borges L., Kubin M., Chin W., Peterson L.,
RA Hsu M.L.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells from Tonsils;
RA Strausberg R.;

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RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF009220; AAB63521.1; -.
DR EMBL: BC015731; AAH15731.1; -.
DR HSSP: P43626; INKR.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR Pfam: PF00047; IG_3.
DR PROSITE: PS00835; IG_LIKE; 2.
KW Receptor.
SQ SEQUENCE 650 AA; 70816 MW; D1321C0982B44BCA CRC64;

Query Match      6.8%; Score 123; DB 4; Length 650;
Best Local Similarity 20.6%; Pred. No. 0.0098;
Matches 68; Conservative 39; Mismatches 105; Indels 118; Gaps 12;

QY 51 VRLEVTGPPATPAYWDGEKEVLAVARGAPALLTCVNRGHVWTDHVEEAQQVHWDROP 110
DB 326 VLSVQPGP-----TVASGENVTLCCSQGMQFTLTKEGAADPW----- 367
QY 111 PGVPHDRADRLDLVYASGERAYGFLRDRVAVGADAFERGFSLRIEPLVEADEGTY 170
DB 368 -----RLRSTYQSQKYQAEFFM-----GPTVSAHAGTYR 396
QY 171 CH---LHHYCGLHERRVFLHTVAEPHAEPPRPGSGNGSHSGAGPDPTLARGHNVIN 227
DB 397 CYGSSQSKPYLLTHPSDPLELVSGSGGP---SSPTTGTSTSGPEDQLPTGSD--- 450
QY 228 VIVPES--RAHFFQQLGYVLTALLFILLVTLAARRRGYGYEYSDQSGKSGKDVN 285
DB 451 ---PQSGLGRHLGVIGILVAVILLLLLLFLLRHRQGHWTSTQRK----- 498
QY 286 LAEFAVAAG-----DQMLYRS-----EDIQLDYKN----- 310
DB 499 -ADFQHPAGAVGPEPTDRGLQWRSSPAADAQENLYAAVKHTQPEDGVEMDTRSPHDEDP 557
QY 311 -----NILKERAELAH--SPLPAKYID 330
DB 558 QAVTYAEVKHSRPRREMASPPSLSGEFLD 587

RESULT 10
O8NHJ9 PRELIMINARY; PRT; 651 AA.
AC O8NHJ9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Leukocyte immunoglobulin-like receptor-1.
GN LILRB1
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Caravez F.C.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF283985; AAL36989.1; -.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003598; IG_c2.
DR InterPro: IPR003006; IG_MHC.
DR Pfam: PF00047; IG_3.
DR SMART: SM00408; IGC2; 3.
DR PROSITE: PS00835; IG_LIKE; 2.
KW Immunoglobulin domain; Receptor.
SQ SEQUENCE 651 AA; 70906 MW; C85BCCD7CD9996BB CRC64;

Query Match      6.7%; Score 122.5; DB 4; Length 651;
Best Local Similarity 21.9%; Pred. No. 0.011;
Matches 73; Conservative 35; Mismatches 102; Indels 123; Gaps 14;

QY 51 VRLEVTGPPATPAYWDGEKEVLAVARGAPALLTCVNRGHVWTDHVEEAQQVHWDROP 110

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Db 326 VLSVQFGP-----TVASGENVTLLCQSGMMQTFLLTKGAADPW----- 367
Qy 111 PGVPHDRADLLDYASGERAYGFLFLDRVAVGADAFERGFSLRIEPLVADGTY 170
Db 368 -----RLRSYQSKYQAEFPM-----GPTSAHAGTYR 396
Qy 171 CH---LHHYCGLHRRVHFLTVAEPAHPPRPGSPNG-SSHSGAGPDPPTLARGHVI 226
Db 397 CYGSSQSKPYLLTHPSDPLELVSGSPGPP---SSPTTGTSTAGPEDQPLTPTGSD-- 451
Qy 227 NVIVPES---RAHFFQOLGVVATLFLFLLVAVVLAARRRRGGYVSDQSGSKGKDV 284
Db 452 -----PQSGLRHLGVVIGILVAVILLLLLLFLILRHRRQKHWSTQK----- 499
Qy 285 NLAFAVAAG-----DQMLY-----RSED 303
Db 500 ---ADFHAGAVGPEPTDRGLQWRSSPAADAQENLYAAVXHTQPEDGVEMDTRSPHED 557
Qy 304 IQ-----LQYKNILKERAELAH--SPLPAKYID 330
Db 556 LQAVTYAEVKHS--RPRREMASPPSPLSGEFLD 588

RESULT 11
O75025 PRELIMINARY; PRT; 652 AA.
AC O75025
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Leucocyte immunoglobulin-like receptor-1.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Cosman D., Fanger N., Borges L., Kubin M., Chin W., Peterson L.,
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF009221; AAB63522.1; -.
DR HSSP; P43626; INKR.
DR Genew; HGNC:6605; LILRB1.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG_2.
DR SMART; SM00409; IG_2.
DR PROSITE; PS00835; IG_LIKE; 2.
SQ SEQUENCE 652 AA; 71018 MW; 93AF8F021A22949D CRC64;

Query Match 6.7%; Score 122; DB 4; Length 652;
Best Local Similarity 21.4%; Pred. No. 0.012;
Matches 71; Conservative 37; Mismatches 104; Indels 120; Gaps 13;
Qy 51 VRLVTDGPPATPAYWDGEKEVLAVARGAPALLTCNVRGHVWTDHVEEAQGVHWDQ 110
Db 326 VLSVQFGP-----TVASGENVTLLCQSGMMQTFLLTKGAADPW----- 367
Qy 111 PGVPHDRADLLDYASGERAYGFLFLDRVAVGADAFERGFSLRIEPLVADGTY 170
Db 368 -----RLRSYQSKYQAEFPM-----GPTSAHAGTYR 396
Qy 171 CH---LHHYCGLHRRVHFLTVAEPAHPPRPGSPNG-SSHSGAGPDPPTLARGHVI 226
Db 397 CYGSSQSKPYLLTHPSDPLELVSGSPGPP---SSPTTGTSTAGPEDQPLTPTGSD-- 451
Qy 227 NVIVPES---RAHFFQOLGVVATLFLFLLVAVVLAARRRRGGYVSDQSGSKGKDV 284
Db 452 -----PQSGLRHLGVVIGILVAVILLLLLLFLILRHRRQKHWSTQK----- 499
Qy 285 NLAFAVAAG-----DQMLY-----EDIQDYKNILKE 315

Db 500 ---ADFHAGAVGPEPTDRGLQWRSSPAADAQENLYAAVXHTQPEDGVEMDTRSPHDE 557
Qy 316 -----RAELAH-----SPLPAKYID 330
Db 558 DQAVTYAEVKHSRPRREMASPPSPLSGEFLD 589

RESULT 12
Q8N1C7 PRELIMINARY; PRT; 448 AA.
ID Q8N1C7
AC Q8N1C7
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Leucocyte immunoglobulin-like receptor, subfamily B (With TM and ITIM domains), member 4.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Straussberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC026309; AAB26309.1; -.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG_2.
DR Receptor.
SQ SEQUENCE 448 AA; 49303 MW; A6155D29E7D89812 CRC64;
Query Match 6.6%; Score 120.5; DB 4; Length 448;
Best Local Similarity 21.9%; Pred. No. 0.01;
Matches 87; Conservative 40; Mismatches 131; Indels 139; Gaps 20;
Qy 48 SLAVRLEVTGPPATPAYWDGEKEVLAVARGAPALLTCNVRGHVW-----TDRHVEEA 100
Db 14 SLGPRDQAGLPKFTLWAEFGSVISWG-----NSVTIMCQGTLEAREYLDKE 63
Qy 101 QQVHVHWRDPPGVPHDRA---DRLLDYASGERAY-----GFLFLDRVAVG 145
Db 64 ESPAPWDRQNPLEPKNKARFSPMTEDYA-GRYCYRSPVGSQSPDLEL---VMTG 119
Qy 146 A-----DAF-----ERGDPSL----- 156
Db 120 AYSKPTLSALPSPLVTSGKSVTLCOGRSPMTFTLLIKERAHPLHLRSEHCAQHQAE 179
Qy 157 -RIEPLVADGTYSCHLHH---HYCGLHRRVHFLTVAEPAHPPRPGSPNGSSHGA 212
Db 180 FPMSPVTSVHGTYRCFSSHGFSHYLLSHPSDPLELVS--GSLEGPRSPTRSVSTAAG 237
Qy 213 PGDPTLARGHNVINIVPES---RAHFFQOLGVVATLFLFLLVAVVLAARRRRGGYVSDQSG 260
Db 238 PEDQPLMPTGS-----VPHSGLRHRRHVEVLIGLVVSVILLLLSLLFLLOHNRQGHRTL 291
Qy 261 AAR-----RRRGVEYSQKSG-----KSKGKVNLAEFAVAGDQMLYRSED-IQLDYKN 310
Db 292 AQKQADQFQPPGAEPKDGQGRSSPAADYQGENFCAAVKNT---QPEDGVEMDTRQ 348
Qy 311 NILKE-----RAELAH--SPLPAKYID 330
Db 349 SPHDEDPQAVTYAKVXHSRPRREMASPPSPLSGEFLD 385

RESULT 13
Q8NHL5 PRELIMINARY; PRT; 448 AA.
ID Q8NHL5
AC Q8NHL5
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Leucocyte immunoglobulin-like receptor 5.
GN LIR5.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]

RA MEDLINE=20395285; PubMed=10941817;
 RA Liu W.R., Kim J., Nwankwo C., Ashworth L.K., Arm J.P.;
 RA "genomic organization of the human leukocyte immunoglobulin-like
 RT receptors within the leukocyte receptor complex on chromosome
 RT 19q13.4";
 RL Immunogenetics 51:659-669(2000).

DR EMBL: AF189768; AGO2024.1; --
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00047; ig; 2.
 DR Receptor.
 KW Receptor.

SQ SEQUENCE 448 AA; 49298 MW; 98310C44CEA1993 CRC64;

Query Match 6.6%; Score 119.5; DB 4; Length 448;
 Best Local Similarity 21.9%; Pred. No. 0.013;
 Matches 87; Conservative 39; Mismatches 132; Indels 139; Gaps 20;

QY 48 SLAVRLEVTGDPATPAYWDGKEVLAVARGAPALLTCVNRGHV-----TDRHVEEA 100

DB 14 SLGPRTHMQAGPLPKPTLWAEPSGVISWG-----NSVTIMCQGTLEAREYRLDKE 63

QY 101 QVVVHWDROPVGVPHDRA---DRLLDLVAGSERRAY-----GPLFLDRVAVG 145

DB 64 ESPAPWDRQNPLEPKKNAFSPMTEDYA-GRYCYIYSPVWGSOPSPLEL---VMTG 119

QY 146 A-----DAF-----RGDFSL----- 156

DB 120 AYSKPTLSALPSPLVTSKGSVTLCCQSRSPMDTFLIKERAAPLHLHLEHGAQHQAE 179

QY 157 -RIEPLVADEGNYSCHLHH---HYCGLHERRVFLHTVAEPHAEPPRPGSPGSGSHGA 212

DB 180 FPMSPVTSVHGYYRCFSHGSHGSHYLLSHPSDPLELIVS--GSLEGRSPSTRSVSTAAG 237

QY 213 PGDPPTLARGHNVINVIIPES---RAHFFQOLGYVLATLLLFILLVTVL-----L 260

DB 238 PEDQPLMPTGS-----VPHSGLRHWEVLIGVLVSVILLSLLFLQLQHWKRGKHTL 291

QY 261 AAR---RRGGVEYSDQSG-----KSKGKVNLAFAVAAGDQMLYSED-IQLDYKN 310

DB 292 AQQAQDFQRPQGAEPKDGGLQRRSSPAADQGENFCAVKNV---QPDGVEMDTRQ 348

QY 311 NILKE-----RAELAH-----SPLPAKYID 330

DB 349 SPHEDEPQAVTYAEVXHSRPRREMASPPSPLSGEFLD 385

RESULT 14

ID Q8NHKO PRELIMINARY; PRT; 651 AA.

AC Q8NHKO;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Leukocyte immunoglobulin-like receptor-1.

GN LILRB1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RA Canavez F.C.;

RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF283984; AAL36988.1; --

DR InterPro; IPR007110; ig-like.

DR InterPro; IPR003598; IG_c2.

DR InterPro; IPR003006; IG_MHC.

DR Pfam; PF00047; ig; 3.

DR SMART; SM00408; IGC2; 3.
 DR PROSITE; PS50835; IG_LIKE; 2.
 KW Immunoglobulin domain; Receptor.
 SQ SEQUENCE 651 AA; 70890 MW; 7D4F9D838D844AA6 CRC64;

Query Match 6.6%; Score 119.5; DB 4; Length 651;
 Best Local Similarity 21.1%; Pred. No. 0.021;
 Matches 70; Conservative 36; Mismatches 104; Indels 119; Gaps 13;

QY 51 VRLEVTGDPATPAYWDGKEVLAVARGAPALLTCVNRGHVWTDHRHVEEAQVQVHWDROP 110

DB 326 VLSVQPGP-----TVASGNNVTLCCSQGQNMQTFLLTKGAADDPW---- 367

QY 111 PGVPHDRADLLLYASGERRAYGPLFLDRVAVGADAFERGFSLRIEPLVADCTYS 170

DB 368 -----RURSTYQSKYCAEFPM-----GPTSHAGTYR 396

QY 171 CH---LHHYCYGLHERRVFLHTVAEPHAEPPRPGSPGNG-SSHGAPGPDPTLARGHNV 226

DB 397 CYGQSQSKPYLLTHPSDPLELVWSPSGGP---SSPTTGPTSTAGPEDQPLTPTGSD-- 451

QY 227 NVIIPES---RAHFFQOLGYVLATLLLFILLVTVLAARRRGYVEYSDQSKSGKGDV 284

DB 452 ----PQSLGRHLGVVIGILVAVILLLELLLELLFLILRHRQGHWTSTORK----- 499

QY 285 NLAEFAVAAG-----DQMLYRS-----EDIOLDYKN----- 310

DB 500 --ADFQHPAGAVGPEPTDRGLQWRSSPAADAQENLYAAVKHTQPDGVEMDTRSPHED 557

QY 311 -----NILKERAELAH---SPLPAKYID 330

DB 558 PQAVTYAEVXHSRPRREMASPPSPLSGEFLD 588

RESULT 15

ID C015468 PRELIMINARY; PRT; 448 AA.

AC C015468;

DT 01-JAN-1998 (TrEMBLrel. 05, Created)

DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Monocyte inhibitory receptor precursor.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RA Arm J.P., Nwankwo C., Austen K.F.;

RA "Molecular identification of a novel family of human immunoglobulin

RT superfamily members that possess immunoreceptor tyrosine-based

RT inhibitory motifs and homology to the mouse gp49BI inhibitory

RT receptor.";

RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; U91925; AAB68665.1; --

DR HSSP; P43626; INKR.

DR Genew; HGNC:6508; LILRB4.

DR InterPro; IPR003599; IG_MHC.

DR InterPro; IPR003006; IG_c2.

DR SMART; SM00409; IG; 1.

DR Receptor; Signal.

FW SIGNAL 1 23 POTENTIAL.

FT CHAIN 24 448 MONOCYTE INHIBITORY RECEPTOR.

SQ SEQUENCE 448 AA; 49297 MW; 76D1E2482EA1399 CRC64;

Query Match 6.5%; Score 118.5; DB 4; Length 448;
 Best Local Similarity 21.9%; Pred. No. 0.016;
 Matches 87; Conservative 39; Mismatches 132; Indels 139; Gaps 20;

QY 48 SLAVRLEVTGDPATPAYWDGKEVLAVARGAPALLTCVNRGHVW-----TDRHVEEA 100

DB 14 SLGPRTHMQAGPLPKPTLWAEPSGVISWG-----NSVTIMCQGTLEAREYRLDKE 63

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OM protein - protein search, using sw model

Run on: February 13, 2004, 15:30:52 ; Search time 21 Seconds
(without alignments)
1561.596 Million cell updates/sec

Title: US-10-006-818A-77

Perfect score: 1816

Sequence: 1 MALPSRILLKLVLLQSSAV.....SPLPAKYIDLDKGFRENCK 341

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	113	6.2	1896	2 T08851	Down syndrome cell
2	112	6.2	404	1 I61596	advanced glycosyla
3	111.5	6.1	233	2 JC5322	p53 specific singl
4	105	5.8	423	2 T29549	hypothetical prote
5	105	5.8	1273	2 T42405	sax-3 protein - Ca
6	104.5	5.8	365	2 JC7780	coxsackie- and ade
7	104	5.7	111	2 E53285	Ig kappa chain v a
8	100.5	5.5	246	2 T01073	T cell surface gly
9	100.5	5.5	498	2 S11246	LAG-3 protein prec
10	100.5	5.5	2222	2 T13924	sdh protein - fru
11	99.5	5.5	111	2 D45722	anti-glycoprotein
12	99.5	5.5	246	2 D46482	T-cell surface gly
13	99	5.5	310	2 D70745	hypothetical prote
14	98	5.4	358	2 A54265	CCAAT/enhancer-bin
15	97.5	5.4	1021	2 I39207	leukocyte surface
16	97	5.3	394	2 A70979	hypothetical prote
17	97	5.3	3198	2 A43426	collagen alpha 2 f
18	96.5	5.3	321	2 D39371	Ig V-region-like B
19	96.5	5.3	1033	2 S19247	cell adhesion prot
20	96.5	5.3	1070	2 JC4593	protein-tyrosine k
21	96	5.3	224	2 I37243	CMRP-35 antigen -
22	96	5.3	841	2 JC5894	killer cell inhibi
23	95.5	5.3	210	2 E46482	T-cell surface gly
24	95.5	5.3	221	2 C46482	T-cell surface gly
25	95.5	5.3	1232	2 T43027	neural cell adhesi
26	95	5.2	1268	1 A39640	neural cell adhesi
27	94.5	5.2	240	2 A39016	T-cell surface gly
28	94	5.2	95	2 S25177	Ig kappa chain v r
29	94	5.2	2761	2 T29285	hypothetical prote

30 93.5 5.1 101 2 S59640 Ig light chain v r
31 93.5 5.1 1051 2 A39712 kinase-like protei
32 93.5 5.1 3707 2 S18252 heparan sulfate pr
33 93 5.1 105 2 S44125 Ig lambda chain v
34 93 5.1 129 2 S44114 Ig heavy chain v r
35 93 5.1 395 2 I49575 CCAAT/enhancer bin
36 92.5 5.1 102 2 PH1077 Ig light chain v r
37 92.5 5.1 111 2 A33936 Ig kappa chain v r
38 92.5 5.1 303 2 S23440 hypothetical prote
39 92.5 5.1 340 2 JC7505 brain link protein
40 92.5 5.1 4391 2 A38096 perlecan precursor
41 92 5.1 461 1 A46077 steroid hormone re
42 92 5.1 1344 2 T14316 rig-1 protein - mo
43 91.5 5.0 111 1 KVMS13 Ig kappa chain v r
44 91.5 5.0 115 2 S63596 Ig kappa chain v r
45 91.5 5.0 131 1 KVMSM6 Ig kappa chain pre

ALIGNMENTS

RESULT 1

Down syndrome cell adhesion protein 1 - human (fragment)
N/Alternate names: Down syndrome cell adhesion molecule
C/Species: Homo sapiens (man)
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C/Accession: T08851
R.Yamakawa, K.; Huo, Y.K.; Haendel, M.A.; Hubert, R.; Chen, X.N.; Lyons, G.E.; Korenber
submitted to the EMBL Data Library, September 1997
A/Description: DSCAM: A novel member of the immunoglobulin superfamily maps in a down s
A/Reference number: Z16495
A/Accession: T08851
A/Status: preliminary; translated from GE/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1896 <YAM>
A/Cross-references: EMBL:AF023449; NID:G3169765; PID:G3169766
A/Experimental source: Brain; developmental stage: 14 weeks; fetal
C/Genetics:
A/Gene: DSCAM
A/Map position: 21q22
A/Note: derived from alternatively-spliced mRNA
C/Function:
A/Description: involved in nervous system development
C/Keywords: alternative splicing

Query Match 6.2%; Score 113; DB 2; Length 1896;
Best Local Similarity 23.0%; Pred. No. 0.6;
Matches 45; Conservative 33; Mismatches 62; Indels 56; Gaps 9;

Qy 11 KLVLLQSSAVLLHSABEETDAGLYTGNLHHY-----CHLYESLAVRLEVTGPPATPAY 65
Db 728 RIQVLSGSLIKHVVVEE-DSGYLCKVNDVGADVSKSMYLTVKTPAMITSYNTLAT 786
Qy 66 WDGEKSLVAVGAPALLTCVNRGHVWTDHRVFEAQOVVHWDQRPQGVPHDRADRLDLY 125
Db 787 QGQKKEMSCXTAHG-----EKPIIVRWEXE-----DRIIN-- 815
Qy 126 ASGERRAYGLFLFDRVA---VGADAPERGDFSLRIEPLVADGTYSCHLHHYCOLHE 182
Db 816 -----PEMARLYLSTKEGVEVIS-----TLQLFTVREDSGFFSCHAINSYG--ED 860
Qy 183 RRVFHLTVASPHAPPP 198
Db 861 RGIQLTVQEP-PDPP 875

RESULT 2

I61596
advanced glycosylation end-products receptor precursor - human
N/Alternate names: advanced glycosylation end product-binding protein, 35K; glycoprotein
C/Species: Homo sapiens (man)
C/Date: 24-May-1996 #sequence_revision 07-Feb-1997 #text_change 16-Jul-1999

C;Accession: I61596; B42879; S27968
R;Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko, H.;
Genomics 23, 408-419, 1994
A;Title: Three genes in the human MHC class III region near the junction with the class
II part of mouse mammary tumor gene int-3.
A;Reference number: A55562; MUID:95137587; PMID:7835890
A;Accession: I61596
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
A;Molecule type: DNA
A;Residues: 1-404 <RES>
A;Cross-references: GB:D28769; NID:9561657; PIDN:BAA05958.1; PID:9561659
R;Nepper, M.; Schmidt, A.M.; Brett, J.; Yan, S.D.; Wang, F.; Pan, Y.C.; Elliston, K.; S
J. Biol. Chem. 267, 14998-15004, 1992
A;Title: Cloning and expression of a cell surface receptor for advanced glycosylation en
A;Reference number: A42879; MUID:92340547; PMID:1378843
A;Accession: B42879
A;Molecule type: mRNA
A;Residues: G, 2-99, R, 101-404 <NEE>
A;Cross-references: EMBL:M91211; NID:gl90845; PIDN:AAA03574.1; PID:gl90846
A;Experimental source: lung
A;Note: sequence extracted from NCBI backbone (NCBIP:109438)
C;Comment: Advanced glycosylation end products are heterogeneous nonenzymatically glycos
cellular function, thus contributing to tissue lesions in diabetes.
C;Comment: This receptor appears also to mediate the effects of amyloid beta peptide on
aces in the neurotoxic pathway that produces dementia in Alzheimer's disease.
C;Genetics:
A;Gene: GDB:AGER
A;Cross-references: GDB:306354; OMIM:600214
A;Map position: 6p21.3-6p21.3
A;Introns: 18/1, 53/3, 119/1, 140/3, 170/1, 231/1, 274/3, 322/1, 331/1, 373/2
C;Function:
A;Description: neuronal receptor for amphoterin, a DNA-binding protein involved in neur
C;Superfamily: advanced glycosylation end products receptor; immunoglobulin homology
C;Keywords: Alzheimer's disease; glycoprotein; receptor; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-404/Product: advanced glycosylation end products receptor #status predicted <MAT>
F;23-344/Domain: extracellular #status predicted <EXT>
F;31-101/Domain: immunoglobulin homology <IM1>
F;137-210/Domain: immunoglobulin homology <IM2>
F;252-303/Domain: immunoglobulin homology <IM3>
F;345-362/Domain: transmembrane #status predicted <TM>
F;363-404/Domain: intracellular #status predicted <INT>
F;25.81/Binding site: carbohydrate (Asn) #status predicted
F;38-99,144-208,259-301/Disulfide bonds: #status predicted

Query Match 6.2%; Score 112; DB 1; Length 404;
Best Local Similarity 21.5%; Pred. No. 0.12;
Matches 85; Conservative 39; Mismatches 109; Indels 162; Gaps 18;

QY 4 PSRIILWKI-----VLLQSAVLLHSAVEETDAGLYTCN-L 38
Db 45 PPRLEWKLTGRTEANKVLSPOGGPMDSVARVLPNGSLFL--PAVGIQDEGIFRCQAM 102
QY 39 HHHYCHLYESLAVRLVETDGPATPAYWDGKEVLAVARGAPALL--TCVNRGHV----- 91
Db 103 NRGKETSINRYRVYQI---PKPEI VDSASELTA---GVNPKVGTCTVSEGSYPAGTLS 156
QY 92 W-----TDRHVE-----EAQVV-----HWDRQP-----PGVPH 115
Db 157 WHLDGKPLVPNEKGVSKVEQTRHPETGLFTLQSELMTVPARGGDPRTFSCSPGLPR 216
QY 116 DRADRLLDLYAGERRAYGFLFDRVAV-----GADAFERGFSLRIE----- 159
Db 217 HRAALTAPI-----QPRWVEFVLEEVQVVEGAVAPGGVTTLTCEVPAQPSQIHMM 272
QY 160 ----PLEV-----ADEGTYSCHLHHYHCGLHERRVFLTVAEPHASPPTGRGS 202
Db 273 KGVPLPLPSPVLLILPEIGPDQGTYSVCVATHSSHGQESRAVSISIIPEEGPTAGS 332
QY 203 PNGSSHSAGAPDDPTLARGHNVINVIPESRAHFQQLGVYATLLFLI-----L 253
Db 333 VG-----GSLGLTALALGILGLGTAA 355

QY 254 LLVTVLLAARRRRGGYEYSDQKSGKSGKGVNLA 288
Db 356 LLIGVILWQRQRGEE---RKAPENQEEERAE 387

RESULT 3
JC5322
p53 specific single-chain antibody Pab421 - human
C;Species: Homo sapiens (man)
C;Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997
C;Accession: JC5322
R;Jannot, C.B.; Hynes, N.E.
Biochem. Biophys. Res. Commun. 230, 242-246, 1997
A;Title: Characterization of scfv-421, a single-chain antibody targeted to p53.
A;Reference number: JC5322; MUID:97168950; PMID:9016757
A;Accession: JC5322
A;Molecule type: mRNA
A;Residues: 1-233 <JAN>
A;Experimental source: hydrioclonoma cell
C;Comment: This protein specifically binds the tumor suppressor protein p53. It restore

Query Match 6.1%; Score 111.5; DB 2; Length 233;
Best Local Similarity 24.3%; Pred. No. 0.068;
Matches 43; Conservative 22; Mismatches 57; Indels 55; Gaps 6;

QY 17 SSANVLLHSAVEETDAGLYTCNLLHHYCHLYESLAVR-----LEVTDP 59
Db 73 NTAYQLSLTSEDATVYTCNAGMDYWGQITVTYSSGGSGGRASGGSDILTQSP 132
QY 60 PATPAYWDGKEVLAVARGAPALLTCVNRGHVWTDHVEEAQQVNVHWRQPPGVPHDRAD 119
Db 133 AS-----LAVSLQORATISCRASKSVSTSGY-----SYMHNQKFGQP----P 172
QY 120 RLILDLYASGERRAYGFLFDRVAVGADAFERG-----DFSLRIEPLVADSGTYSC 171
Db 173 RLL-----IYLVSNLESGVPAFSGSGSGTDTFLNIHPVEEDATYYC 216

RESULT 4
T29549
hypothetical protein ZK377.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T29549
R;Nhan, M.; Hawkins, J.
submitted to the EMBL Data Library, February 1997
A;Description: The sequence of C. elegans cosmid ZK377.
A;Reference number: Z20639
A;Accession: T29549
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-423 <NHA>
A;Cross-references: EMBL:U88183; PIDN:AAB52658.1; GSPDB:GN00028; CESP:ZK377.3
A;Experimental source: strain Bristol N2; clone ZK377
C;Genetics:
A;Gene: CESP:ZK377.3
A;Map position: X
A;Introns: 24/1; 142/3; 229/3; 284/2; 408/3

Query Match 5.8%; Score 105; DB 2; Length 423;
Best Local Similarity 23.4%; Pred. No. 0.48;
Matches 49; Conservative 27; Mismatches 79; Indels 54; Gaps 9;

QY 15 LQSAVLLHSAVEETDAGLYTCNLLHHYCHLYESLAVRLVETDGPATPAYWDGKEVL 74
Db 183 LHSQDGNLLIIDVDRSDSGTYCCVANNWGVRSNPA-RLSVFEKP-----FEQEPKDMT 236
QY 75 VARGAPALLTCVNRGHVWTDHVEEAQQVNVHWRQPPGVPHDRADRLLDLYASGERRAYG 134
Db 237 VDVGAAVLFDG-----RVTDGDPQLTWKRNKNEPVPTRA-----YIAKDNR--- 278
QY 135 PLFLDRVAVGADAFERGFSLRIEPLVADSGTYSCHLHHYHCGLHERRVFLTVAEP- 193

```

Db 279 -----GLRIERVQPSDEGEYVCYARNP-AGTLEASA-HLRVQAPP 316
Qy 194 --HAEPGRSPGNGSSH-----SGAPGP 215
Db 317 SFOTKPADQSPVAGGTATFECTLVGPSP 345

RESULT 5
T42405
sax-3 protein - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C:Accession: T42405
R:Zallen, J.A.; Yi, B.A.; Bargmann, C.I.
Cell 92, 217-227, 1998
A:Title: The conserved immunoglobulin superfamily member SAX-3/Robo directs multiple asp
A:Reference number: 222160; PMID:96117250; PMID:9458046
A:Accession: T42405
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1273 <ZAL>
A:Cross-references: EMBL:AF041053; NID:G2804779; PIDN:AAC38848.1; PID:G2804780
C:Genetics:
A:Note: sax-3
A:Description: sax-3 function is required at the time of axon guidance

Query Match 5.8%; Score 105; DB 2; Length 1273;
Best Local Similarity 23.4%; Pred. No. 1.7;
Matches 49; Conservative 27; Mismatches 79; Indels 54; Gaps 9;

Qy 15 LQSAVLHSAVETDAGLYTCNLHHYCHLYSLAVRLVETDGPATPAYWDGKEVLA 74
Db 184 LHSQDGLNIIDPVRSDSGTYQCANNVGVRSNPA-RLSVFEKPK-----PEQEPKMT 237
Qy 75 VARGAPALLTCVNRGHVWTDHVEEAQVHVWDRPGVPHDRADRLLDLYASGERRAYG 134
Db 238 VDVGAAVLFDG-----RVGDPQPTWIRKNEPMVTRA-----YIAKNR--- 279
Qy 135 PLFLRDRVAVGADAFERDGSRLRIEPLVADGTYSCHLHHYCHLHRRVFLTVAP- 193
Db 280 -----GLRIERVQPSDEGEYVCYARNP-AGTLEASA-HLRVQAPP 317
Qy 194 --HAEPGRSPGNGSSH-----SGAPGP 215
Db 318 SFOTKPADQSPVAGGTATFECTLVGPSP 346

RESULT 6
JC7780
coxackie- and adenovirus receptor - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 02-Apr-2002
C:Accession: JC7780
R:Roelien, I.; Keyaerts, E.; Lindberg, M.; Van Ranst, M.
Biochem. Biophys. Res. Commun. 288, 805-808, 2001
A:Title: Characterization of a cDNA encoding the bovine coxsackie and adenovirus receptor
A:Reference number: JC7780
A:Contents: Liver
A:Accession: JC7780
A:Molecule type: mRNA
A:Residues: 1-365 <THO>
A:Cross-references: GB:AY033651
C:Comment: This protein serves as the primary adenoviral attachment site on bovine cells

Query Match 5.8%; Score 104.5; DB 2; Length 365;
Best Local Similarity 20.1%; Pred. No. 0.44;
Matches 55; Conservative 48; Mismatches 90; Indels 81; Gaps 13;

Qy 70 KEVLAVARGAPALLTCVNRGHVWTDHVEEAQVHVWDRPGVPHDRADRLDLVYASGE 129
Db 26 EQMLEKAGETAYLPC-----KFTLGPEDQGLDIEWLLSP--ADNKKVDQVILLY-SGD 77

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Qy 130 RRAYCPLF--LRDRVAVGADAFERDGSRLRIEPLVADGTYSCHLHHYCHLHRRVFL 187
Db 78 --KIYDDYYQDLKGRVHFTSNDLKGSDASINVTLNQLSDIGTYQCKV-KKAPGVGNKKIQL 135
Qy 188 LTVAPF-----HAEP-----PPRGPSP 203
Db 136 TVLVKPSGIRCVVDGSEBIGNDFKLKCEPKEGSLPLRYEWQKLSDSQKLPSTWLPENTSP 195
Qy 204 -----GNGSSHGA-----PGDPTLARGHNVINIVPESBAHFPOQLGYVLATILL 250
Db 196 VISVKNASAEYSGYTCVNRVNSDQCLLR-----LDVVPNSRAGTT--AGAVIGITLLA 249
Qy 251 FILLIVTVLLAARRRRRGYBYSDQSKSGKGV 284
Db 250 LVLIATLVFCCHKRR-----EEKYEKVVHDI 277

RESULT 7
ES3285
IG kappa chain V and J regions, monoclonal antibody OHP 4B2.2.1 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C:Accession: ES3285
R:Sawada, J.; Mizusawa, S.; Terao, T.; Naito, M.; Kurosawa, Y.
Mol. Immunol. 28, 1063-1072, 1991
A:Title: Molecular characterization of monoclonal anti-steroid antibodies: primary structure and their pH-reactivity profiles.
A:Reference number: A53285; PMID:92017897; PMID:1922102
A:Accession: ES3285
A:Status: preliminary
A:Molecule type: DNA; protein
A:Residues: 1-111 <SAW>
A:Cross-references: GB:D12731; NID:G220542; PIDN:BA02223.1; PID:G220543
A:Note: sequence extracted from NCBI backbone (NCBIN:63307, NCBI:63311)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMW>

Query Match 5.7%; Score 104; DB 2; Length 111;
Best Local Similarity 29.1%; Pred. No. 0.12;
Matches 34; Conservative 15; Mismatches 40; Indels 28; Gaps 5;

Qy 55 VTDGPPATPAYWDGKEVLAVARGAPALLTCVNRGHVWTDHVEEAQVHVWDRPGV 114
Db 4 VTQSPAS-----LAVSLQRATVSC--RASSVDRY---GNFIHWYQKQGP 47
Qy 115 HDRADRLDLVYASGERRAYGFLFLRDRVAVGADAFERDGSRLRIEPLVADGTYSC 171
Db 48 ----PQLLIYFASNLKSGVPARF-----SGSGSRTDFTLIDPVEADDAATYC 92

RESULT 8
T01073
T cell surface glycoprotein CD8 beta 1 chain, membrane-bound type M-2 - human
C:Species: Homo sapiens (man)
C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 21-Jul-2000
C:Accession: T01073
R:Nakayama, K.; Kawachi, Y.; Tokito, S.; Minami, N.; Yamamoto, R.; Imai, T.; Gachelin, J.
Immunol. 148, 1919-1927, 1992
A:Title: Recent duplication of the two human CD8 beta chain genes.
A:Reference number: A46482; PMID:92176658; PMID:1541829
A:Accession: T01073
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-246 <NAK>
A:Cross-references: EMBL:S87083; NID:G246739; PIDN:AAB21671.2; PID:G5705881
C:Genetics:
A:Gene: CD8-beta.2
A:Introns: 15/1; 135/1; 165/1; 195/1; 207/2
C:Superfamily: T-cell surface glycoprotein CD8 beta chain; immunoglobulin homology

Query Match 5.5%; Score 100.5; DB 2; Length 246;
Best Local Similarity 22.8%; Pred. No. 0.6;

```


A:Molecule type: mRNA
A:Residues: 1-1021 <RES>
A:Cross-references: EMBL:Z33642; NID:9854194; PID:9854195
C:Genetics:
A:Gene: GDB:V7
A:Cross-references: GDB:702141
A:Map position: lp13-lp13
C:Superfamily: human leukocyte surface protein V7

Query Match	5.4%	Score 97.5;	DB 2;	Length 1021;
Best Local Similarity	22.4%	Pred. No. 5.7;		
Matches	72;	Conservative 40;	Mismatches 106;	Indels 103; Gaps 17;

QY	26	VEETDAGLYTCNLHHHYCHLYESLAVLEVTGDPPEAYWD--GEX-----EVLAVARG	78
Db	768	VEDSDRGKYHC-----AVEEMLSTNGTWHKLGEXKSGLTCLKPTG	810
QY	79	APALLTCVNRGHVMTDRHVEAQV-----HWDROPFG---VPHDR	117
Db	811	SKVRVSKV---YWTENVTEHREVAIRCLESVGSATLYSVMYWYNNRENSGSKLLVHLQ	866
QY	118	ADRLDLYASGERRAYGFLFDRVAVGADAFERGFSLRIEPLIEVADEGTYS-----H	172
Db	867	HDGLE-----YGEGLRGHLHCYRSS--STDFVLKLHQVEMEDAGMYCWRVAEWQ	915
QY	173	LHHHYC-GLHERRVPHLTVAEPHAEPPRPGSGNGSGHSGAPGPDPTLARGHNVINVIP	231
Db	916	LHGHPKWKINKHPMSHSGWCSPCCIQSPLPGS-----APRP-PLL-----	956
QY	232	ESRAHFFOOLGYVLATLLFILLVTVLLAARRRRGGYEYSDQKSG--KSKGKDVNLAEF	289
Db	957	-----YF-----LFICPFVLLILLITSLCLYKAR---KLSTLRNTRKEXALWVDLKE-	1003
QY	290	AVAAGDQMLYRSEDIOLDYKN	310
Db	1004	---AGVTTNRREDEEEN	1021

Search completed: February 13, 2004, 15:35:15
Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 13, 2004, 15:16:02 ; Search time 17 seconds
(without alignments)
943.300 Million cell updates/sec

Title: US-10-006-818A-77

Perfect score: 1816

Sequence: 1 MALPSRILLKWLVLQSSAV.....SPLPAKYIDLXGPRKXENCK 341

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	113	6.2	2012	1	DSCA_HUMAN
2	112	6.2	404	1	RAGE_HUMAN
3	108.5	6.0	319	1	A33_HUMAN
4	107.5	5.9	365	1	CD4F_HUMAN
5	104	5.7	458	1	CD4F_HUMAN
6	100.5	5.5	525	1	LAG3_HUMAN
7	99	5.5	310	1	Y497 MYCTU
8	98.5	5.4	300	1	JAM1_MOUSE
9	98	5.4	358	1	CEBA_RAT
10	97	5.3	391	1	P53_MARMO
11	97	5.3	458	1	CD4F_HUMAN
12	97	5.3	458	1	CD4F_HUMAN
13	96.5	5.3	1070	1	PTK7_HUMAN
14	96	5.3	224	1	CM35_HUMAN
15	95.5	5.3	210	1	CD8B_HUMAN
16	95.5	5.3	458	1	CD4F_HUMAN
17	95	5.2	1284	1	NRC1_CHICK
18	94.5	5.2	240	1	CD4F_HUMAN
19	94	5.2	458	1	CD4F_HUMAN
20	93.5	5.1	1051	1	PTK7_CHICK
21	93.5	5.1	3707	1	PGBM_MOUSE
22	93	5.1	359	1	CEBA_MOUSE
23	92.5	5.1	303	1	HYBP_AZOVI
24	92.5	5.1	338	1	LAMP_RAT
25	92.5	5.1	340	1	BRA1_HUMAN
26	92.5	5.1	4391	1	PGBM_MOUSE
27	92	5.1	359	1	LACH_DROME
28	92	5.1	458	1	CD4F_HUMAN
29	92	5.1	461	1	STF1_BOVIN
30	91.5	5.0	111	1	KV3E_MOUSE
31	91.5	5.0	111	1	KV3J_MOUSE
32	91.5	5.0	111	1	KV3K_MOUSE
33	91.5	5.0	131	1	KV3I_MOUSE

ALIGNMENTS

RESULT 1									
ID	DSCA_HUMAN	STANDARD;	PRT;	2012	AA.				
AC	060469; 060468;								
DT	16-OCT-2001 (Rel. 40, Created)								
DT	16-OCT-2001 (Rel. 40, Last sequence update)								
DT	15-SEP-2003 (Rel. 42, Last annotation update)								
DE	Down syndrome cell adhesion molecule precursor (CHD2).								
GN	DSCAM.								
OS	Homo sapiens (Human).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.								
OX	NCBI_TaxID=9606;								
RN	[1]								
RP	SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.								
RC	TISSUE=Brain;								
RX	MEDLINE=98087574; PubMed=9426258;								
RA	Yamakawa K., Huot V.-K., Haendelt M.A., Hubert R., Chen X.-N.,								
RA	Lyons G.E., Korenberg J.R.,								
RT	"DSCAM: a novel member of the immunoglobulin superfamily maps in a								
RT	Down syndrome region and is involved in the development of the								
RT	nervous system."								
RL	Hum. Mol. Genet. 7:227-237(1998).								
RN	[2]								
RP	SEQUENCE FROM N.A., AND FUNCTION.								
RX	MEDLINE=20384934; PubMed=10925149;								
RA	Agarwal K.L., Nakamura S., Tsutsumi Y., Yamakawa K.,								
RT	"Down syndrome cell adhesion molecule DSCAM mediates homophilic								
RT	intercellular adhesion."								
RL	Brain Res. Mol. Brain Res. 79:118-126(2000).								
RN	[3]								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE=2028799; PubMed=10830953;								
RA	Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,								
RA	Park H.-S., Toyoda A., Ishii K., Tokoi Y., Choi D.-K., Groner Y.,								
RA	Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,								
RA	Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,								
RA	Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,								
RA	Rosenwald A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,								
RA	Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,								
RA	Minoshima S., Shimizu N., Nordstiek G., Hornischer K., Brandt P.,								
RA	Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloeker H.,								
RA	Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Daggand E.,								
RA	Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,								
RA	Lehrach H., Reinhardt R., Yaspo M.-L.,								
RT	"The DNA sequence of human chromosome 21."								
RL	Nature 405:311-319(2000).								
CC	!- FUNCTION: CELL ADHESION MOLECULE THAT CAN MEDIATE CATION-								
CC	INDEPENDENT HOMOPHILIC BINDING ACTIVITY. COULD BE INVOLVED IN								
CC	NERVOUS SYSTEM DEVELOPMENT.								
CC	!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (PROBABLE). THE								
CC	SHORT ISOFORM MAY BE SECRETED.								
CC	!- ALTERNATIVE PRODUCTS:								
CC	Event-Alternative splicing; Named isoforms=2;								
CC	Name=Long; Synonyms=CHD2-52;								
CC	isoId=060469-1; Sequence=Displayed;								

34	91	5.0	129	1	HV2F_HUMAN	P01824	homo sapien
35	91	5.0	526	1	BUTY_HUMAN	Q13410	homo sapien
36	90.5	5.0	210	1	CD8B_PONPY	P30434	pongo pygma
37	90.5	5.0	298	1	JAM1_BOVIN	Q9xt56	bos taurus
38	90.5	5.0	764	1	ICCR_DROME	Q08180	drosophila
39	90.5	5.0	806	1	CEK2_CHICK	P18460	gallus gall
40	90	5.0	416	1	RAGE_BOVIN	Q28173	bos taurus
41	90	5.0	458	1	CD4_HUMAN	P01730	homo sapien
42	89.5	4.9	111	1	KV3R_MOUSE	P01671	mus musculus
43	89.5	4.9	111	1	KV3S_MOUSE	Q96n03	homo sapien
44	89.5	4.9	204	1	CTX2_HUMAN	Q12644	neurospora
45	89.5	4.9	219	1	NUIM_NEUCR		

QY 92 W-----TDRHVE-----EAQVV-----HWDROP-----EGVPH 115
Db 157 WHLDKGLVNEKGVSKVETRRPPTGLTLOGLAVTTPARGDPRPTSCSFSPGLR 216
QY 116 DRARLDLYASGERAYGPIFLDRVAV-----CADAFGRDPSLRTE----- 159
Db 217 HRLARTAPI-----QPRVNEPVLBEVQLWVEPEGAVAGTGTTLTCEVPAQSPQIHM 272
QY 160 -----PLEV-----ADGTYSCHLHHYCGLHERRVPHLTVABPHAEPPRGS 202
Db 273 KDGVPPLPPSPVLLPIELGPDQGTSCVATHSHGPFQSRVAVSIIIEPGEETAGS 332
QY 203 PONGSSHSGACGPDPTLARGHNVINIVPESRAHFFQOLGVLTALLFI-----L 253
Db 333 VG-----GSGLGTALALGILGLGTAA 355
QY 254 LLVTVLLAARRRGYEDSKSGKGDVNLAE 288
Db 356 LLIGVILWQRQRGEE---RKAPENQEEERAE 387
RESULT 3
A33_HUMAN STANDARD; PRT; 319 AA.
AC Q99795;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Cell surface A33 antigen precursor (Glycoprotein A33).
GN GPA33.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Colon carcinoma;
RX MEDLINE=97165045; PubMed=9012807;
RA Heath J.K., White S.J., Johnston C.N., Catimel B., Simpson R.J.,
RA Moritz R.L., Tu G.-F., Ji H., Whitehead R.H., Groenen L.C.,
RA Scott A.M., Ritter G., Cohen L., Welt S., Old L.J., Nice E.C.,
RA Burgess A.W.;
RT "The human A33 antigen is a transmembrane glycoprotein and a novel
RT member of the immunoglobulin superfamily."
RL Proc. Natl. Acad. Sci. U.S.A. 94:469-474 (1997).
RN [2]
RP POST-TRANSLATIONAL MODIFICATIONS.
RX MEDLINE=97396159; PubMed=9245713;
RA Ritter G., Cohen L.S., Nice E.C., Catimel B., Burgess A.W.,
RA Moritz R.L., Ji H., Heath J.K., White S.J., Welt S., Old L.J.,
RA Simpson R.J.;
RT "Characterization of posttranslational modifications of human A33
RT antigen, a novel palmitoylated surface glycoprotein of human
RL gastrointestinal epithelium."
RL Biochem. Biophys. Res. Commun. 236:682-686 (1997).
CC -!- FUNCTION: MAY PLAY A ROLE IN CELL-CELL RECOGNITION AND SIGNALING.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN NORMAL GASTROINTESTINAL
CC EPITHELIUM AND IN 95% OF COLON CANCERS.
CC -!- PTM: N-GLYCOSYLATED, CONTAINS APPROXIMATELY 8 KDA OF N-LINKED
CC CARBOHYDRATE.
CC -!- PTM: PALMITOYLATED.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC
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DR EMBL; U79725; AAC50957.1; -.
DR Genew; HGNC:4445; GPA33.
DR MIM; 602171; -.
DR GO; GO:0005888; C:proteoglycan integral to plasma membrane; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
KW Immunoglobulin domain; Lipoprotein; Palmitate; Glycoprotein;
KW Transmembrane; Signal; Antigen.
FT SIGNAL 1 21
FT CHAIN 22 319 CELL SURFACE A33 ANTIGEN.
FT DOMAIN 22 235 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 236 256 POTENTIAL.
FT DOMAIN 257 319 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 22 134 IG-LIKE V-TYPE.
FT DOMAIN 140 227 IG-LIKE C2-TYPE.
FT DOMAIN 258 261 POLY-CYS.
FT DISULFID 43 117 POTENTIAL.
FT DISULFID 146 222 POTENTIAL.
FT DISULFID 162 211 POTENTIAL.
FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 319 AA; 35632 MW; 9BFC7AAF45C2408E CRC64;
Query Match 6.0%; Score 108.5; DB 1; Length 319;
Best Local Similarity 25.6%; Pred. No. 0.074; 79; Indels 33; Gaps 10;
Matches 50; Conservative 33; Mismatches 33;
QY 45 LYESLAVRLEVDGPPATPAYWDGEKEVLAVARGAPALLTCYNRGHVWTRHVEAQVV 104
Db 9 LWTLCARVTVDAISVETP-----QDVLRASQGSVTLPCY---HTST---SSREGLI 56
QY 105 HNDROPFGVPHDRDLDDLYASGERAYGPIFLDRVAVGADAPERGFSLRPLEVA 164
Db 57 QMDK-----LLLTHTRWVWIPFSPKNYIHGELY-KNRVSIISNNA-EQSDASITDOLTWA 110
QY 165 DECTYSC--HLHHYCGLHERRVPHLTVABPHAEPPRGPNG-----SSHQA 212
Db 111 DNGTYCSVLSMSDLGNTKSRVLLVLP--SKPECGIEGETIIGNNIQLTCSKEGS 168
QY 213 PGDPPTLARGHNVIN 227
Db 169 PTPQYSWKR-YNINL 182
RESULT 4
CXAR_HUMAN STANDARD; PRT; 365 AA.
ID CXAR_HUMAN
AC P78310; O00694;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Cxsackievirus and adenovirus receptor precursor (Cxsackievirus B-
DE adenovirus receptor) (hCAR) (CVB3 binding protein).
GN CXADR OR CAR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97190109; PubMed=9036860;
RA Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E.,
RA Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W.;
RT "Isolation of a common receptor for Cxsackie B viruses and
RT adenoviruses 2 and 5."
RL Science 275:1320-1323 (1997).
RN [2]

SEQUENCE FROM N.A.
 RA Tomko R.P., Xu R., Philipson L.;
 RA "HCAR and MCRAR: the human and mouse cellular receptors for subgroup C
 RT adenoviruses and group B coxsackieviruses.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356(1997).
 [3]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20008750; PubMed=10543405;
 RA Bowles K.R., Gibson J., Wu J., Shaffer L.G., Towbin J.A.,
 RA Bowles N.E.;
 RT "Genomic organization and chromosomal localization of the human
 RT coxsackievirus B-adenovirus receptor gene.";
 RL Hum. Genet. 105:354-359(1999).
 [4]
 RP SEQUENCE FROM N.A.
 RA Anderson C.W., Kieleczawa J., Dunn J.J., Freimuth P.;
 RA "Sequence and expression of CXADR, the human gene for the
 RT coxsackievirus and adenovirus receptor.";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 [5]
 RP SEQUENCE FROM N.A.
 RA Anderson B., Tomko R., Andersson K., Darban H., Oncu D., Mizra M.,
 RA Sollerbrant K., Sonhammer E., Philipson L.;
 RA "Putative regulatory domains in the human and mouse CAR genes.";
 RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [6]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cervix;
 RA MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Dratchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: SERVES AS A RECEPTOR FOR GROUP B COXSACKIEVIRUSES AND
 CC SUBGROUP C OF ADENOVIRUSES (AD2 AND AD5).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
 CC
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 DR EMBL; Y07593; CAA68868.1; -;
 DR EMBL; U90716; AAC51234.1; -;
 DR EMBL; AF169366; AAF05908.1; JOINED.
 DR EMBL; AF169360; AAF05908.1; JOINED.
 DR EMBL; AF169361; AAF05908.1; JOINED.
 DR EMBL; AF169362; AAF05908.1; JOINED.
 DR EMBL; AF169363; AAF05908.1; JOINED.
 DR EMBL; AF169364; AAF05908.1; JOINED.
 DR EMBL; AF169365; AAF05908.1; JOINED.
 DR EMBL; AF200465; AAF24344.1; -;

DR EMBL; AF242865; AAG01088.1; -;
 DR EMBL; AF242862; AAG01088.1; JOINED.
 DR EMBL; AF242864; AAG01088.1; JOINED.
 DR EMBL; EC003684; AAH03684.1; -;
 DR EMBL; BC010536; AAH10536.1; -;
 DR PDB; 1EAJ; 13-JUL-01.
 DR PDB; 1F5W; 08-NOV-99.
 DR PDB; 1KAC; 24-NOV-99.
 DR Genew; HGNC:2559; CXADR.
 DR MIM; 602621; -;
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0004872; F:receptor activity; TAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig C2.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig_2.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PS00835; IG_LIKE; 2.
 DR Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
 KW Repeat; 3D-structure.
 FT SIGNAL 1 19
 FT CHAIN 20 365
 FT DOMAIN 20 237
 FT TRANSMEN 238 258
 FT DOMAIN 259 365
 FT DOMAIN 20 134
 FT DOMAIN 141 228
 FT DISULFID 41 120
 FT DISULFID 162 212
 FT CARBOHYD 106 106
 FT CARBOHYD 201 201
 FT SEQUENCE 365 AA; 40029 MW; AS01C6346CB7FE64 CRC64;
 SQ
 Query Match 5.9%; Score 107.5; DB 1; Length 365;
 Best Local Similarity 19.3%; Pred. No. 0.11;
 Matches 53; Conservative 48; Mismatches 92; Indels 81; Gaps 12;
 QY 70 KEVLAVARGAALLTCVNRGHVWDRHVEEAQQVHVHWDROPVPHDRADLLDYASGE 129
 Db 26 BEMIEKAGETAYLPC-----KFTLSPEDQGLDIEWLSP--ADNQKVDQVILY-SGD 77
 QY 130 RRAYGPIF--LRDRVAVGADAFERGFSLRIEPLVEADGTYCHLHHYHGLHRRVFH 187
 Db 78 -KIYDDYVPLDKGRVHFTSNLKGSDASINVNLQLSDIGTYQCKV-KKAPGVANKKIHL 135
 QY 168 LTVAEPAHAE-----PPRGS----- 202
 Db 136 VLVKPSGARCYVDGSEIEGSDFKIKCEPKEGSLPQVEWQKLSDSQKMPFSLAEMTSS 195
 QY 203 ----PGNGSSHSGA-----PGPDPTLARGHNVINIVIPESRAHFQQLGYVLATILL 250
 Db 196 VISVKNASSEYSGTYGTCVNRVSGDQCLLR-----LNVVPPSNKAGLI--AGAIIGTLA 249
 QY 251 FILLVTVLLAARRRGYGYSDQKSGSKGKV 284
 Db 250 LALIGLIIFCCKRR-----EKYEKVVHDI 277
 RESULT 5
 ID CD4_MACNE STANDARD; PRT; 458 AA.
 AC Q08340; P79196;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE T-cell surface glycoprotein CD4 precursor (T-cell surface antigen
 DE T4/Leu-3).
 GN CD4
 OS Macaca nemestrina (Pig-tailed macaque).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Cercopithecidae; Macaca.
 OC NCBI_TaxID=9545;

```

RN  SEQUENCE FROM N.A.
RA  Hashimoto O., Tatsumi M.;
RL  Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
[2]
RP  SEQUENCE OF 28-424 FROM N.A.
RC  TISSUE=Blood; PubMed=1425921;
RX  MEDLINE=93045640; PubMed=1425921;
RA  Fongsgaard A., Hirsch V.M., Johnson P.R.;
RT  "Cloning and sequences of primate CD4 molecules: diversity of the
RT  cellular receptor for simian immunodeficiency virus/human
RT  immunodeficiency virus."
RL  Eur. J. Immunol. 22:2973-2981(1992).
CC  -!- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL
CC  RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION.
CC  -!- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
CC  -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC  -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC  -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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CC  -----
CC  EMBL; D63346; BAA09670.1; -
CC  EMBL; X73325; CAA51751.1; -
CC  HSP; P01730; IWR.
CC  GO; GO:0042101; C: T-cell receptor complex; ISS.
CC  GO; GO:0015026; P: coreceptor activity; ISS.
CC  GO; GO:0042289; P: MHC class II protein binding activity; ISS.
CC  GO; GO:0006955; P: immune response; ISS.
CC  GO; GO:0045085; P: positive regulation of interleukin-2 biosyn. . . ; ISS.
CC  GO; GO:0030211; P: T-cell differentiation; ISS.
CC  GO; GO:0045058; P: T-cell selection; ISS.
CC  GO; GO:0007169; P: transmembrane receptor protein tyrosine kin. . . ; ISS.
CC  InterPro; IPR000973; CD4 TCAG.
CC  InterPro; IPR003006; IG_MHC.
CC  InterPro; IPR003596; IG_V.
CC  Pfam; PF00047; igf.2.
CC  PRINTS; PRC0692; CD4TCANTIGEN.
CC  SMART; SM00406; IGV. 1.
CC  PROSITE; P850835; IG_LIKE; 1.
KW  Immunoglobulin domain; Transmembrane; Glycoprotein; T-cell;
KW  Immune response; Repeat; Signal; Lipoprotein; Palmitate.
FT  SIGNAL 1 25
FT  CHAIN 26 458
FT  DOMAIN 26 396
FT  TRANSMEM 397 418
FT  DOMAIN 419 458
FT  DOMAIN 26 125
FT  DOMAIN 126 203
FT  DOMAIN 204 317
FT  DOMAIN 318 374
FT  CARBOHYD 318 42
FT  CARBOHYD 296 325
FT  CARBOHYD 325 325
FT  DISULFID 41 109
FT  DISULFID 155 184
FT  DISULFID 328 370
FT  LIPID 419
FT  LIPID 422 422
FT  CONFLICT 57 91
FT  CONFLICT 91 91
FT  CONFLICT 105 105
FT  CONFLICT 113 113
FT  CONFLICT 302 302
FT  CONFLICT 349 349
SQ  SEQUENCE 458 AA; 50905 MW; 751A9BA2C8B3BE16 CRC64;

Query Match 5.7%; Score 104; DB 1; Length 458;
Best Local Similarity 22.7%; Pred. No. 0.28; Indels 72; Gaps 12;
Matches 59; Conservative 35; Mismatches 94; Indels 72; Gaps 12;

QY 63 PAYWDGEKEVLAVARGAPALLTCVNRGHWTDRLHVEEAQQVHVHDROPQPPGVPHDRRL 122
DB 20 PAVTQGGKVLG-KKGDVETLC-----NASQKNTQFHW-----KNSDQIK 60
QY 123 DIYASGERRAYGPLELDRVAVGADAFERGFSLRIEPLVADGTYSCHLHHVYGLHE 182
DB 61 ILGIQGSFLTKGPKSLSDRADSRKSLWQGGCFSMIIRKIKIEDSNITYICEVENEKEV-E 119
QY 183 RRVFILTVAEPH-----AEPFPRGSPGNGSSHGAPDPPTLARGHNVINIVP 231
DB 120 LLVFGLTANSRTHLLEGQSLTLTLESPPGSSP---SVKCRSPG-----GKNI----- 163
QY 232 ESRAHFFQGLGVVATLLIFILLVTLVLAARRRGVEYS---DQSGKSGKGVNLAE 288
DB 164 -----QGGRTLSVPQL-----ERQDSGTWTCTVSDQKTVEFK---IDIV 201

RESULT 6
LAG3 HUMAN STANDARD; PRT; 525 AA.
ID LAG3 HUMAN
AC P18627;
DT 01-NOV-1990 (Rel. 16, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Lymphocyte activation gene-3 protein precursor (LAG-3) (FDC protein)
DE (CD223 antigen).
GN LAG3 OR FDC
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID:9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90237736; PubMed=1692078;
RA Triebel F., Jitsukawa S., Baixeras E., Roman-Roman S., Genevee C.,
RA Viegas-Pequignot E., Hercend T.;
RT "LAG-3, a novel lymphocyte activation gene closely related to CD4.";
RL J. Exp. Med. 171:1393-1405(1990).
[2]
RP REVISIONS TO C-TERMINUS.
RA Triebel F.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
[3]
RP CHARACTERIZATION.
RX MEDLINE=92364535; PubMed=1380059;
RA Baixeras E., Huard B., Miossec C., Jitsukawa S., Martin M.,
RA Hercend T., Aufray C., Triebel F., Platier-Ronneau D.;
RT "Characterization of the lymphocyte activation gene 3-encoded
RT protein. A new ligand for human leukocyte antigen class II
RT antigens.";
RL J. Exp. Med. 176:327-337(1992).
CC -!- FUNCTION: INVOLVED IN LYMPHOCYTE ACTIVATION. BINDS TO HLA CLASS-II
CC ANTIGENS.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: ON CELL SURFACE OF ACTIVATED NK AND
CC T-LYMPHOCYTES.
CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- DATABASE: NAME=PROW; NOTE=PROW 3:15-18(2002);
CC WWW="http://www.ncbi.nlm.nih.gov/blast/blast.cgi?seq1=1656481751.g.htm"
CC
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EWEL; X51985; CAA36243.3; --
 DR EMBL; A21353; CAA01547.1; ALT_SEQ.
 DR Genew; HGNC:6476; LAG3.
 DR MIM; 153337; --
 DR GO; GO:0003823; F:antigen binding activity; TAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR003006; IG_YHC.
 DR Pfam; PF00047; IG; 3.
 DR SMART; SM00409; IG; 3.
 DR PROSITE; PS00835; IG-LIKE; 2.
 KW Signal; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat.
 FT SIGNAL 1 28
 FT CHAIN 29 525 LYPHOCYTE ACTIVATION GENE-3 PROTEIN.
 FT DOMAIN 29 450 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 451 471
 FT DOMAIN 472 525
 FT CYTOPLASMIC (POTENTIAL).
 FT IG-LIKE V-TYPE.
 FT DOMAIN 37 167
 FT DOMAIN 168 252 IG-LIKE C2-TYPE 1.
 FT DOMAIN 265 343 IG-LIKE C2-TYPE 2.
 FT DOMAIN 348 419 IG-LIKE C2-TYPE 3.
 FT POTENTIAL.
 FT DISULFID 44 160
 FT DISULFID 189 241
 FT DISULFID 282 333
 FT DISULFID 369 412
 FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 250 250 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 256 256 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 343 343 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 525 AA; 57436 MW; C711EDB03E2733 CRC64;

Query Match 5.5%; Score 100.5; DB 1; Length 525;
 Best Local Similarity 26.6%; Pred. No. 0.65;
 Matches 46; Conservative 9; Mismatches 69; Indels 49; Gaps 5;
 QY 60 PATPAYWDGKEVLAVARGAPALLTC-----VNRGHVWTRDHVEEAQVHVWDR 108
 DB 19 PVKPLQGAEPVWVWAGEAPALQPCSPPTLPDLSLRAG-----VTWQH 65
 QY 109 QP-----PGV-----PHDRADRLDLYASGERRAYGFLFDRVAVG 145
 DB 66 QPDSGPPAAAPGHLAPGHPAAPSMSGPRPRRYTVLSVGPGLRS--GRLLPQPRVQLD 123
 QY 146 ADAFERGDFSLRIEPLVADGTYSCHLHHYCGLHERRVFLHTVAEPHREPP 198
 DB 124 ERGRQGFSLWLPARRADAGEYRAAVHLDRALSCLRLRLGQASMTASPP 176

RESULT 7
 Y497 MYCTU
 ID Y497 MYCTU STANDARD; PRT; 310 AA.
 AC Q11162;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical protein RV0497.
 GN RV0497 OR MT0517 OR MTCY20G9.23.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OK NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RX MEDLINE=98259587; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekoaia P.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.";
 RL Nature 393:537-544 (1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Esmolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weyman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains";
 RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
 CC -|- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -|- SIMILARITY: TO M.LEPRAE ML2433.
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EMBL; 277162; CAB00923.1; --
 EMBL; AE006952; AAK44740.1; --
 PIR; D70745; D70745.
 TIGR; MT0517; --
 DR Tuberculist; RV0497; --
 KW Hypothetical protein; Transmembrane; Complete proteome.
 FT TRANSMEM 231 251
 FT TRANSMEM 257 277
 FT TRANSMEM 286 306
 FT DOMAIN 33 39
 FT DOMAIN 197 202
 FT POLY-ALA.
 SQ SEQUENCE 310 AA; 33092 MW; 4954027F694DF5C2 CRC64;

Query Match 5.5%; Score 99; DB 1; Length 310;
 Best Local Similarity 22.5%; Pred. No. 0.45;
 Matches 67; Conservative 35; Mismatches 92; Indels 104; Gaps 16;
 QY 39 HHY---CHLYESLAV--RLEVTGPPATPAYWDGKEVLAVARGAPALLTCVNRGHVWT 93
 DB 61 HHAGPDHAGSQSPAANGRVGVGEAATQSPA-----EPVA----- 95
 QY 94 DRHVEEAQVHVWD-----RQPPGVPHDRADRLDLYASGERRAYGFLFDRVAVG 145
 DB 96 EQVAEEPTRTVYVQSPEPRWPKSPQDRRE-----SGPELSEYPRPLRHTHSDRAPAG 148
 QY 146 ADAFERGDFSLRIEPLVADGTYSCHLHHYCGLHERRVFLHTVAEPHREPPR-GSPG 204
 DB 149 PPS---GAHMSPPDVE-----HYPLWV-DVLDTEVGEAEETEVEAQPQ 191
 QY 205 NGSSH--SGAPGPD-----PTLARGHNV--NVIVPESRAHFFQQL 241
 DB 192 RGERHAAAAAGTVEGDGAARVARRALDVVFTLWRGALVTLQSLAVAFAGAGLFI 251
 QY 242 GYV-----LATLLIFILLVTVLLAARRRGVBYSDQSKSGKGVNLAEPFAVAG 294
 DB 252 DQLWRNSIVALVLSVMVILGVSVRAVR-----KTEDASTLLI 296

RESULT 8
 JAM1 MOUSE
 ID JAM1 MOUSE STANDARD; PRT; 300 AA.
 AC O88732.
 DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Junctional adhesion molecule 1 precursor (JAM).
 GN F11R OR JAM1 OR JCAM1 OR JCAM.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98327120; PubMed=9660867;
 RA Martin-Padura I., Lostaglio S., Schneemann M., Williams L., Romano M.,
 RA Fruscella P., Panzeri C., Stoppacciaro A., Ruco L., Villa A.,
 RA Simmons D., Dejana E.;
 RT "Junctional adhesion molecule, a novel member of the immunoglobulin
 RT superfamily that distributes at intercellular junctions and modulates
 RT monocyte transmigration.";
 RL J. Cell Biol. 142:117-127(1998).
 RN [2]
 RP INTERACTION WITH PAR3.
 RX PubMed=11447115;
 RA Ebnat K., Suzuki A., Horikoshi Y., Hirose T.,
 RA Meyer zu Brucke M.-K., Ohno S., Vestweber D.;
 RT "The cell polarity protein ASIP/PAR-3 directly associates with
 RT junctional adhesion molecule (JAM).";
 RL EMBO J. 20:3738-3748(2001).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 212-238.
 RX PubMed=11500366;
 RA Kostrewa D., Brockhaus M., D'Arcy A., Dale G.E., Melboeck P.,
 RA Schmid G., Mueller F., Bazzoni G., Dejana E., Bartfai T.,
 RA Winkler F.K., Hennig M.;
 RT "X-ray structure of junctional adhesion molecule: structural basis for
 RT homophilic adhesion via a novel dimerization motif.";
 RL EMBO J. 20:4391-4398(2001).
 CC -1- FUNCTION: Seems to play a role in epithelial tight junction
 CC formation. Appears early in primordial forms of cell junctions and
 CC recruits PAR3. The association of the PAR3-PAR3 complex may
 CC prevent the interaction of PAR3 with JAM1, thereby preventing
 CC tight junction assembly. Plays a role in regulating monocyte
 CC transmigration involved in integrity of epithelial barrier.
 CC Involved in platelet activation.
 CC -1- SUBUNIT: Interacts with the first PDZ domain of PAR3. The
 CC association between PAR3 and PAR3B probably disrupts this
 CC interaction.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC Localized at tight junctions of both epithelial and endothelial
 CC cells.
 CC -1- TISSUE SPECIFICITY: Localized at tight junctions of both
 CC epithelial and endothelial cells.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -1- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
 CC
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 CC
 CC EMBL; U89915; AAC32982.1; -;
 CC PDB; 1F97; 22-AUG-01.
 CC MGD; MGI:1321398; F11r.
 CC DR InterPro; IPR007110; Ig-like.
 CC DR InterPro; IPR003006; Ig_MHC.
 CC DR InterPro; IPR003596; Ig_V.
 CC DR Pfam; PF00047; Ig; 2.
 CC DR SMART; SMC0406; IGV; 1.
 CC DR PROSITE; PS50835; IG_LIKE; 2.
 CC Tight junction; Immunoglobulin domain; Glycoprotein; Transmembrane;
 KW Repeat; Signal; 3D-structure.
 FT SIGNAL 1 26
 FT
 FT CHAIN 27 300 JUNCTIONAL ADHESION MOLECULE 1.
 FT DOMAIN 27 238 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 239 259 POTENTIAL.
 FT DOMAIN 260 299 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 28 122 IG-LIKE V-TYPE 1.
 FT DOMAIN 134 230 IG-LIKE V-TYPE 2.
 FT DISULFID 49 108 POTENTIAL.
 FT DISULFID 152 212 POTENTIAL.
 FT CARBOHYD 42 42 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 300 AA; 32368 MW; 391P3E48FFB3B97EC CRC64;
 Query Match 5.4%; Score 98.5; DB 1; Length 300;
 Best Local Similarity 21.9%; Pred. No. 0.48;
 Matches 59; Conservative 27; Mismatches 104; Indels 79; Gaps 11;
 QY 17 SSALLHSAVEETDAGLYTCNLHHYCHLYSEAVLRLEVTDCGPATPAYWDGKEVLAVA 76
 DB 89 SSGITFSSVTRKDNGEYTCVSEGGQNYGEVSHLTVL-VPPSKPTI----- 136
 QY 77 RGAPALLTCVNRGHVWTDNRHVEEAQOVVHWDRQPPGVPHDRADRLDLVASGER-RAYGP 135
 DB 137 -SVESVTTIGNRAVLTCSEH-----DGSPFSEYSWFKDGISMLTADAKTRA--- 182
 QY 136 LFLDRVAVGADAFERGFSLRIEPLLEVADEGTYSCHLHHYCGLHERRVFLTVAEPA 195
 DB 183 -FMNSFTIDP---KSGD--LIFDPVTFDSSEYICQAGQNGYGTAMRSEAHDVAE--- 233
 QY 196 EPPRSGPNSGSHSGAPGDPPTLARGHNVINIVPESRAHFFQQLGYVLATLLFILL 255
 DB 234 -----LNVGGIVAA-----VLVTLLILGLLI 254
 QY 256 VTLLAARRRGVEYSDQSKSGSKGV 284
 DB 255 FGWVFAYSR---GY-FETTKGTAPGKKV 279
 RESULT 9
 CEBA RAT
 ID -CEBA RAT STANDARD; PRT; 358 AA.
 AC P05554;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE CCAAT/enhancer binding protein alpha (C/EBP alpha).
 GN CEPA.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 253-269.
 RX STRAIN=Sprague-Dawley;
 RX MEDLINE=89092001; PubMed=2850264;
 RA Landschulz W.H., Johnson P.F., Adashi E.Y., Graves B.J.,
 RA McKnight S.L.;
 RT "Isolation of a recombinant copy of the gene encoding C/EBP.";
 RL Genes Dev. 2:786-800(1988).
 RN [2]
 RP REVISIONS. SEQUENCE FROM N.A.
 RX STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=95011606; PubMed=7926792;
 RA Lincoln A.J., Williams S.C., Johnson P.F.;
 RT "A revised sequence of the rat c/ebp gene.";
 RL Genes Dev. 8:1131-1132(1994).
 CC -1- FUNCTION: C/EBP IS A DNA-BINDING PROTEIN THAT RECOGNIZES TWO
 CC DIFFERENT MOTIFS: THE CCAAT HOMOLGY COMMON TO MANY PROMOTERS AND
 CC THE ENHANCED CORE HOMOLGY COMMON TO MANY ENHANCERS.
 CC -1- SUBUNIT: BINDS DNA AS A DIMER AND CAN FORM STABLE HETERODIMERS
 CC WITH C/EBP BETA AND GAMMA.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: Belongs to the bZIP family. C/EBP subfamily.
 CC

DE T4/Leu-3).

GN CD4

OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecoidea; Macaca.

OX NCBI_TaxID=9541;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Thymocytes;

RA Tatsumi M., Yabe M., Yamada Y.K.;

RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL

CC RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION.

CC -!- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.

CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.

CC

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CC

CC EMBL; D63349; BAA09673.1; -.

CC HSSP; P01730; 1WBR.

CC GO; GO:0042101; C:T-cell receptor complex; ISS.

CC GO; GO:0015026; F:MHC class II protein binding activity; ISS.

CC GO; GO:0042289; P:MHC class II protein binding activity; ISS.

CC GO; GO:0006955; P:immune response; ISS.

CC GO; GO:0045086; P:positive regulation of interleukin-2 biosyn. . . ; ISS.

CC GO; GO:0030217; P:T-cell differentiation; ISS.

CC GO; GO:0045058; P:T-cell selection; ISS.

CC GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . . ; ISS.

CC InterPro; IPR000973; CD4 TCAG.

CC InterPro; IPR007110; Ig-Like.

CC InterPro; IPR003006; Ig-MHC.

CC InterPro; IPR003596; Ig_V.

CC Pfam; PF00047; 1g; 2.

CC PRINTS; PR00692; CD4TCANTIGEN.

CC SMART; SM00406; IG; 1.

CC KX Immunoglobulin domain; Transmembrane; Glycoprotein; T-cell;

FT SIGNAL

FT CHAIN

FT DOMAIN

FT TRANSMEM

FT DOMAIN

FT DOMAIN

FT DOMAIN

FT DOMAIN

FT CARBOHYD

FT CARBOHYD

FT CARBOHYD

FT DISULFID

FT DISULFID

FT DISULFID

FT LIPID

FT LIPID

SQ SEQUENCE 458 AA; 50872 MW; 9105479FB5C56FF7 CRC64;

Query Match

Best Local Similarity 22.3%; Pred. No. 1.1;

Matches 58; Conservative 36; Mismatches 72; Gaps 12;

QY 63 PAYVDEKEVLAVARGAPALLTTCVNRGHVWTDHVEAQVHWDQPGVPHDRADRL 122

DB 20 PAVTQGGKVVLG-KKGTVELTC-----NASQKNTQFHW-----KNSNQIK 60

QY 123 DLYASGERAYGFLFLDRVAVGADAFERGFSLRIEPLVADGTYSCHLHHYGLHE 182

DB 61 ILGIQSGFLTKGFSKLSRADSRKSLWDQCFSMIKNLKIEDSDTYICEVENKKEEV-E 119

QY 183 RRVFHLTV-AEPH-----AEPFPGSGNGSHSGAGPDPPTLARGHNVINVIP 231

DB 120 LNVFGLTANSDDLHLEQSLTLTLESPPGSSP---SVKCRSPG-----GKNI 163

QY 232 ESRAHFQQLGVYVATLLLFILLVTLVLAARRRGYEYS---DQKSGSKGKDVNLAE 288

DB 164 -----QGRTLSVPQL-----ERQDSGTWCTVSDQDKTVEFK---IDIVV 201

QY 289 FAVAAGDQMLYRSEDQLDY 308

DB 202 LAFQKASSTVYKKEGQVEF 221

RESULT 12

CD4_MACFU STANDARD; PRT; 458 AA.

AC P95184; 1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE T-cell surface glycoprotein CD4 precursor (T-cell surface antigen

DE T4/Leu-3).

GN CD4.

OS Macaca fuscata fuscata (Japanese macaque).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecoidea; Macaca.

OX NCBI_TaxID=9543;

RN [1]

RP SEQUENCE FROM N.A.

RA Hashimoto O., Tateuchi M.;

RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL

CC RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION.

CC -!- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.

CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.

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CC

CC EMBL; D63348; BAA09672.1; -.

CC HSSP; P01730; 1WBR.

CC GO; GO:0042101; C:T-cell receptor complex; ISS.

CC GO; GO:0015026; F:coreceptor activity; ISS.

CC GO; GO:0042289; P:MHC class II protein binding activity; ISS.

CC GO; GO:0006955; P:immune response; ISS.

CC GO; GO:0045086; P:positive regulation of interleukin-2 biosyn. . . ; ISS.

CC GO; GO:0030217; P:T-cell differentiation; ISS.

CC GO; GO:0045058; P:T-cell selection; ISS.

CC GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . . ; ISS.

CC InterPro; IPR000973; CD4 TCAG.

CC InterPro; IPR007110; Ig-Like.

CC InterPro; IPR003006; Ig-MHC.

CC InterPro; IPR003596; Ig_V.

CC Pfam; PF00047; 1g; 2.

CC PRINTS; PR00692; CD4TCANTIGEN.

CC SMART; SM00406; IG; 1.

CC KX Immunoglobulin domain; Transmembrane; Glycoprotein; T-cell;

FT SIGNAL

FT CHAIN

FT DOMAIN

FT TRANSMEM

FT DOMAIN

FT DOMAIN

FT DOMAIN

FT CARBOHYD

FT CARBOHYD

FT CARBOHYD

FT DISULFID

FT DISULFID

FT DISULFID

FT LIPID

FT LIPID

SQ SEQUENCE 458 AA; 50872 MW; 9105479FB5C56FF7 CRC64;

Query Match

Best Local Similarity 22.3%; Pred. No. 1.1;

Matches 58; Conservative 36; Mismatches 72; Gaps 12;

QY 63 PAYVDEKEVLAVARGAPALLTTCVNRGHVWTDHVEAQVHWDQPGVPHDRADRL 122

DB 20 PAVTQGGKVVLG-KKGTVELTC-----NASQKNTQFHW-----KNSNQIK 60

FT CHAIN 26 458 T-CELL SURFACE GLYCOPROTEIN CD4.
 FT DOMAIN 26 396 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 397 418 POTENTIAL.
 FT DOMAIN 419 458 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 26 125 IG-LIKE V-TYPE.
 FT DOMAIN 126 203 IG-LIKE C2-TYPE 1.
 FT DOMAIN 204 317 IG-LIKE C2-TYPE 2.
 FT DOMAIN 318 374 IG-LIKE C2-TYPE 3.
 FT CARBOHYD 42 42 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
 FT CARBOHYD 325 325 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
 FT DISULFID 41 109 BY SIMILARITY.
 FT DISULFID 155 184 BY SIMILARITY.
 FT DISULFID 328 370 BY SIMILARITY.
 FT LIPID 419 419 PALMITATE (BY SIMILARITY).
 FT LIPID 422 422 PALMITATE (BY SIMILARITY).
 SQ SEQUENCE 458 AA; 50828 MW; 76B3E7EF08185535 CRC64;
 Query Match 5.3%; Score 97; DB 1; Length 458;
 Best Local Similarity 21.9%; Pred. No. 1.1;
 Matches 57; Conservative 35; Mismatches 96; Indels 72; Gaps 12;
 QY 63 PAYWDGEKVLAVARGAPALITCVNRGHVHTDRHVEAQVWHDROPVGVPHDRADRL 122
 DB 20 PAVTQGGKVVLG-KKGDVTVELTC-----NASQKNTQPHW-----KNSNQIK 60
 QY 123 DLYASGERRAYGFLFLDRVAVGADAFERGFSLRIEPIEVADEGTYSCHLHHYCGLHE 182
 DB 61 ILGTQGSFLTKGPSKLSRADRSKSLWDQCFSMIKNLIEDSDTYICEVENKKEV-E 119
 QY 183 RVPHLTV-REPH-----AEPPIRGSPNGSHSGAGPDPTLARGHNV---INV 228
 DB 120 LLVFLGTANSDFHLLGQSLTLTESPPGSSP---SVKCRSPG-----GKNIQGGRTI 169
 QY 229 IVPESRAHFFQOLGYVLATLLFLLLVTLAARRRRGGYVSDOKSGSKCKDYNLA 288
 DB 170 SVPLER---QDSTWTCV-----SQDQKTVPEFK---IDIVV 201
 QY 289 FAVAAGDMLYRSEDIDLY 308
 DB 202 LAFQKASSTVYKKEGEQVEF 221
 RESULT 13
 PTK7_HUMAN
 ID_PTK7_HUMAN STANDARD; PRT; 1070 AA.
 AC Q13308; Q13417;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tyrosine-protein kinase-like 7 precursor (Colon carcinoma kinase-4)
 DE (CKK-4).
 GN PTK7 OR CKK4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon carcinoma, and Placenta;
 RX MEDLINE=96074849; PubMed=7478540;
 RA Mossie K., Jallal B., Alves F., Sures I., Plowman G.D., Ullrich A.;
 RT "Colon carcinoma kinase-4 defines a new subclass of the receptor
 tyrosine kinase family";
 RL Oncogene 11:2179-2184(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fibroblast;
 RX MEDLINE=97037064; PubMed=8882711;
 RA Park S.-K., Lee H.-S., Lee S.-T.;
 RT "Characterization of the human full-length PTK7 cDNA encoding a
 receptor protein tyrosine kinase-like molecule closely related to
 chick KLG.";

RL J. Biochem. 119:235-239 (1996).
 [3]
 RN SEQUENCE FROM N.A., AND REVISION TO 834.
 RA Lee S.-T., Park S.-K., Lee H.-S., Ji A.R., Jung J.W.;
 RL Submitted (Nov-2001) to the EMBL/GenBank/DDAJ databases.
 CC -!- FUNCTION: MAY FUNCTION AS A CELL ADHESION MOLECULE. LACKS PROBABLY
 THE CATALYTIC ACTIVITY OF TYROSINE KINASE. MAY BE CONNECTED TO THE
 PATHOPHYSIOLOGY OF COLON CARCINOMAS AND/OR MAY REPRESENT A TUMOR
 PROGRESSION MARKER.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG, LIVER, PANCREAS,
 KIDNEY, PLACENTA AND MELANOCYTES. WEAKLY EXPRESSED IN THYROID
 GLAND, OVARY, BRAIN, HEART AND SKELETAL MUSCLE. ALSO EXPRESSED IN
 ERYTHROLEUKEMIA CELLS. BUT NOT EXPRESSED IN COLON.
 CC -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. INSULIN
 RECEPTOR SUBFAMILY.
 CC -!- SIMILARITY: Contains 7 immunoglobulin-like C2-type domains.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; U33635; AA87565.1; -;
 DR EMBL; U40271; AAC50484.2; -;
 DR EMBL; AF447176; AAL39062.1; -;
 DR EMBL; AF447157; AAL39062.1; JOINED.
 DR EMBL; AF447158; AAL39062.1; JOINED.
 DR EMBL; AF447162; AAL39062.1; JOINED.
 DR EMBL; AF447164; AAL39062.1; JOINED.
 DR EMBL; AF447167; AAL39062.1; JOINED.
 DR EMBL; AF447170; AAL39062.1; JOINED.
 DR EMBL; AF447171; AAL39062.1; JOINED.
 DR EMBL; AF447173; AAL39062.1; JOINED.
 DR EMBL; AF447174; AAL39062.1; JOINED.
 DR EMBL; AF447175; AAL39062.1; JOINED.
 DR HSSP; F08631; IAD5.
 DR Genew; HGNC:9618; PTK7.
 DR MIM; 601890; -;
 DR GO; GO:0005885; C:plasma membrane; TAS.
 DR GO; GO:0005888; C:proteoglycan integral to plasma membrane; TAS.
 DR GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG_c2.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002011; RtkinaseII.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00047; Ig; 7.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00408; IGC2; 5.
 DR SMART; SM00219; Tyrc; 1.
 DR PROSITE; PS50835; IG_LIKE; 7.
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
 DR PROSITE; PS00239; RECEPTOR TYR KIN II; FALSE NEG.
 KW Receptor; Transmembrane; signal; Glycoprotein; Cell adhesion;
 KW Immunoglobulin domain; Repeat.
 FT SIGNAL 1 30 POTENTIAL.
 FT CHAIN 31 1070 TYROSINE-PROTEIN KINASE-LIKE 7.
 FT DOMAIN 31 704 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 705 725 POTENTIAL.
 FT DOMAIN 726 1070 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 31 120 IG-LIKE C2-TYPE 1.
 FT DOMAIN 128 218 IG-LIKE C2-TYPE 2.
 FT DOMAIN 225 317 IG-LIKE C2-TYPE 3.
 FT DOMAIN 309 407 IG-LIKE C2-TYPE 4.


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FT DOMAIN 412 497 IG-LIKE C2-TYPE 5.
FT DOMAIN 503 586 IG-LIKE C2-TYPE 6.
FT DOMAIN 578 660 IG-LIKE C2-TYPE 7.
FT DOMAIN 796 1066 PROTEIN KINASE; INACTIVE.
FT DISULFID 53 101 BY SIMILARITY.
FT DISULFID 150 200 BY SIMILARITY.
FT DISULFID 246 301 BY SIMILARITY.
FT DISULFID 343 391 BY SIMILARITY.
FT DISULFID 433 481 BY SIMILARITY.
FT DISULFID 524 570 BY SIMILARITY.
FT DISULFID 613 664 BY SIMILARITY.
FT CARBOHYD 116 116 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 116 116 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 175 175 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 184 184 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 214 214 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 268 268 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 283 283 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 405 405 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 567 567 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 646 646 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 92 92 P -> R (IN REF. 2 AND 3).
FT CONFLICT 147 147 K -> T (IN REF. 2 AND 3).
FT CONFLICT 207 207 S -> G (IN REF. 2 AND 3).
FT CONFLICT 495 496 VL -> RV (IN REF. 2 AND 3).
FT CONFLICT 515 515 G -> B (IN REF. 2 AND 3).
FT CONFLICT 881 881 E -> G (IN REF. 2 AND 3).
FT CONFLICT 969 969 A -> P (IN REF. 2 AND 3).
FT CONFLICT 992 992 S -> F (IN REF. 2 AND 3).
FT SEQUENCE 1070 AA; 118260 MW; 47CDP2588E3698A5 CRC64;

Query Match. 5.3%; Score 96.5; DB 1; Length 1070;
Best Local Similarity 21.8%; Pred. No. 3.4;
Matches 59; Conservative 34; Mismatches 89; Indels 89; Gaps 13;

QY 18 SAVLLHSA-VEETDAGLYTC---NLHHYCHLYESLAVLEVTDPDPATPAWDGKEVL 73
DB 551 NAGTLHFARTRDDAGNYTCIASNGPQGIARHVQLTVAVFT-----FKVEPERT 601
QY 74 AVARGAPALLTCVNRGVHWTDRHVEEAQVHWDRQPPGVPHDRADRLDLVYSGERRAY 133
DB 602 TVYQGHALLQCEAQQ-----DPKPLIQWKGK-----DRILL----- 633
QY 134 GPFLFDRVAVGADAFERGFSLRIEPLVABEGTY-----SCHLHHYCGLHERRVPH 187
DB 634 -PTKLGPRMHI-----FQNG--SLVHIDVAPEDSGRYTCIAGNSCNKIKTEAPLY----- 680
QY 188 LTVAEPAHPPPRPGSPGNGSHSGAPGPPDPTLARGHNVINIVPESRAHFFFOGLGYVLAT 247
DB 681 --VVD---KVPESSEGPQS-----PPP-----YKMIQTIGLSVGA 711
QY 248 LLLFILLVTLVLLAARRRGVYSQKSGK 278
DB 712 AVAYITAVLGLMFYCKKCKAKRLQKPEGE 742

RESULT 14
CM35 HUMAN STANDARD; PRT; 224 AA.
AC Q08708;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE CMRF35 antigen precursor (CMRF-35).
GN CMRF35 OR CMRF35A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=52249405; PubMed=1349532;
RA Jackson D.G., Hart D.N.J., Starling G., Bell J.I.;
```

```
RT "Molecular cloning of a novel member of the immunoglobulin gene
RT superfamily homologous to the polymorphic immunoglobulin receptor.";
RT Eur. J. Immunol. 22:1157-1163(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21442079; PubMed=11556966;
RA Clark G.J., Cooper B., Fitzpatrick S., Green B.J., Hart D.N.;
RA "The gene encoding the immunoregulatory signaling molecule CMRF-35A
RT localized to human chromosome 17 in close proximity to other members
RT of the CMRF-35 family.";
RT Tissue Antigens 57:415-423(2001).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman A., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -1- TISSUE SPECIFICITY: PRESENT ON THE SURFACE OF MONOCYTES.
CC NEUTROPHILS, A PROPORTION OF PERIPHERAL BLOOD T AND B LYMPHOCYTES
CC AND LYMPHOCYTIC CELL LINES.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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CC -----
CC EMBL; X66171; CAA46948.1; --
CC EMBL; AF373866; AAK64272.1; --
CC EMBL; AF373863; AAK64272.1; JOINED.
CC EMBL; AF373864; AAK64272.1; JOINED.
CC EMBL; AF373865; AAK64272.1; JOINED.
CC EMBL; BC022279; AAK22279.1; --
CC PIR; I37243; I37243.
CC MIM; 606786; --
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:0004888; F:transmembrane receptor activity; TAS.
CC GO; GO:0006968; P:cellular defense response; TAS.
CC InterPro; IPR007110; IG-like.
CC InterPro; IPR003599; IG.
CC InterPro; IPR003006; IG_MHC.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00409; IG; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
KW Antigen; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 224 CMRF35 ANTIGEN.
FT DOMAIN 21 183 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 184 204 POTENTIAL.
FT DOMAIN 205 224 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 22 130 IG-LIKE V-TYPE.
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FT DOMAIN 123 175 PRO-RICH.
FT DISULFID 43 110 POTENTIAL.
FT DISULFID 57 65 POTENTIAL.
FT CARBOHYD 90 90 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 99 99 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 224 AA; 24830 MW; 60C88716D84600D2 CRC64;

Query Match 5.3%; Score 96; DB 1; Length 224;
Best Local Similarity 26.6%; Pred. No. 0.54;
Matches 50; Conservative 26; Mismatches 80; Indels 32; Gaps 11;

Qy 106 WDROPPGVHADRLLDLVASERRAYGFLFDRVAVGADAFERGDPSLRIEPLEVAD 165
Db 56 WCR-PPQIL--RCDKIVETGSGAKR--NGRVSIRDSFA-----NLSEFTVTLENLTED 104
Qy 166 EGYTSCHLHHYCCGHE--RRVHLTVAEPHAPPPRGSPGNGSSHS--GAPGPDPTLAR 221
Db 105 AGTY-----WGVDTPLWLRDFADPIVEVSFFAGITTASSPOSSWGTSQP-PTKLP 156
Qy 222 GH---NVINIVPESRAH---FFQQLGYVLATLL---LFILLVTVLLAARRRRGGYYS 272
Db 157 VHTWPSVTRKDSPEPSHPGSLFSNVRFLLLVLELPLLLSMLGAVLWVNRPPQRSRQ 216
Qy 273 DQSKGSK 280
Db 217 NWPKGENQ 224

RESULT 15
CD8B HUMAN
ID CD8B HUMAN STANDARD; PRT; 210 AA.
AC P10966; P14860; P14861; Q9UQ55;
DT 01-JUN-1989 (Rel. 11, Created)
DT 01-JUN-1989 (Rel. 11, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE T-cell surface glycoprotein CD8 beta chain precursor (Antigen CD8B).
GN CD8B1 OR CD8B.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RC TISSUE=T-cell;
RX MEDLINE=89091085; PubMed=3145195;
RA Norment A.M., Littman D.R.;
RT "A second subunit of CD8 is expressed in human T cells.";
RL EMBO J. 7:3433-3439(1988).
[2]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=89091089; PubMed=3145196;
RA Disanto J.P., Knowles R.W., Flomenberg N.;
RT "The human LYT-3 molecule requires CD8 for cell surface expression.";
RL EMBO J. 7:3465-3470(1988).
[3]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=89067811; PubMed=3264320;
RA Shiue L., Gorman S.D., Parnes J.R.;
RT "A second chain of human CD8 is expressed on peripheral blood lymphocytes.";
RL J. Exp. Med. 168:1993-2005(1988).
[4]
RN SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4).
RX MEDLINE=92176658; PubMed=1541829;
RA Nakayama K., Kawachi Y., Tokito S., Minami N., Yamamoto R.,
RA Inai T., Gachelin G., Nakauchi H.;
RT "Recent duplication of the two human CD8 beta-chain genes.";
RL J. Immunol. 148:1919-1927(1992).
CC -!- FUNCTION: IDENTIFIES CYTOTOXIC/SUPPRESSOR T-CELLS THAT INTERACT
CC WITH MHC CLASS I BEARING TARGETS. CD8 IS THOUGHT TO PLAY A ROLE IN
CC THE PROCESS OF T-CELL MEDIATED KILLING.
CC -!- SUBUNIT: IN GENERAL HETERODIMER OF AN ALPHA AND A BETA CHAIN
CC LINKED BY TWO DISULFIDE BONDS.

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-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ISOFORM 3 SEEMS TO BE SECRETED.
 -!- ALTERNATIVE PRODUCTS:
 Event-Alternative splicing; Named isoforms=4;
 Name=1; Synonyms=M-1;
 IsoId=P10966-1; Sequence=Displayed;
 Name=2; Synonyms=M-3;
 IsoId=P10966-2; Sequence=VSP_002490;
 Name=3; Synonyms=M-1;
 IsoId=P10966-3; Sequence=VSP_002492, VSP_002493;
 Name=4; Synonyms=M-2;
 IsoId=P10966-4; Sequence=VSP_002491;
 -!- PTM: PHOSPHORYLATED AS A CONSEQUENCE OF T-CELL ACTIVATION (POSSIBLE).
 -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 -!- DATABASE: NAME=PRO; NOTE=CD guide CD8b entry;
 WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd8beta.htm".

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EMBL; X13444; CRA31795.1; -
 EMBL; X13445; CRA31796.1; -
 EMBL; X13446; CRA31797.1; -
 EMBL; X13452; CRA31803.1; -
 EMBL; Y00805; CRA68750.1; -
 EMBL; M36712; AAA35664.1; -
 EMBL; S87090; AAB21669.2; -
 EMBL; S87068; AAB21669.2; JOINED.
 EMBL; S87070; AAB21669.2; JOINED.
 EMBL; S87073; AAB21669.2; JOINED.
 EMBL; S87081; AAB21670.2; JOINED.
 EMBL; S87083; AAB21671.2; -
 EMBL; S87087; AAB21670.2; -
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 EMBL; S87078; AAB21672.2; JOINED.
 EMBL; S87081; AAB21672.2; JOINED.
 PIR; S01647; E45482.
 PIR; S01873; C45482.
 PIR; S01874; B45482.
 PIR; T01073; T01073.
 Genew; HGNC:1707; CD8B1.
 MIM; 186730; -
 GO; GO:0005887; C: integral to plasma membrane; TAS.
 GO; GO:0042101; C: T-cell receptor complex; NAS.
 GO; GO:0015036; F: coreceptor activity; NAS.
 GO; GO:0042288; F: MHC class I protein binding activity; NAS.
 GO; GO:0005515; F: protein binding activity; IPI.
 GO; GO:0006955; P: immune response; NAS.
 GO; GO:0042110; P: T-cell activation; NAS.
 GO; GO:0007169; P: transmembrane receptor protein tyrosine kin. .; NAS.
 InterPro; IPR007110; Ig-like.
 InterPro; IPR003599; IG.
 InterPro; IPR003006; IG_MHC.
 Pfam; PF00047; Ig; 1.

DR SMART; SMO0409; IG; 1.
KW PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin domain; Transmembrane; T-cell; Antigen; Glycoprotein;
KW Immune response; Signal; Alternative splicing; Phosphorylation.
FT SIGNAL 1 21
FT CHAIN 22 210 T-CELL SURFACE GLYCOPROTEIN CD8 BETA
FT CHAIN
FT DOMAIN 22 170 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 171 191 POTENTIAL.
FT DOMAIN 192 210 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 22 132 IG-LIKE V-TYPE.
FT DISULFID 41 116 POTENTIAL.
FT CARBOHYD 102 102 N-LINKED (GLCNAC...) (POTENTIAL).
FT MOD_RES 209 209 PHOSPHORYLATION (POTENTIAL).
FT VARSPLIC 208 210 FYK -> LRLHPLEKCSRNDY (in isoform 2).
FT VARSPLIC 208 210 /FTID=VSP 002490.
FT VARSPLIC 210 210 FYK -> KFNIVCLKISGFTCCCFQILQISREYGFVLLQ
FT VARSPLIC 210 210 /FTID=VSP 002491.
FT VARSPLIC 166 195 KDIGO (in isoform 4).
FT VARSPLIC 208 210 Missing (in isoform 3).
FT VARSPLIC 208 210 /FTID=VSP 002492.
FT VARSPLIC 208 210 FYK -> PQGEGISGTFVPCQLHGYSNYTTTSQKLNPWIL
FT VARSPLIC 208 210 /FTID=VSP 002493.
FT VARSPLIC 208 210 KT (in isoform 3).
SQ SEQUENCE 210 AA; 23722 MW; 675AD919585F4B80 CRC64;

Query Match 5.3%; Score 95.5; DB 1; Length 210;
Best Local Similarity 22.5%; Pred. No. 0.55; 96; Indels 65; Gaps 10;
Matches 56; Conservative 32; Mismatches 96;

QY 45 LYESLAVRLVETDGPAA---TPAYWDGKEKVLAVARGAPALLTCVNRGHWTDHRVVEAQ 101
DB 5 LWLLAAQLTVLHGNSVLQQTAY-----IKVQTNKMWMLSC-----EAKISLSN 49
QY 102 QVHWDRQPGVPHDRADLLDIYASGERRAYGFLRDRVAVGADAFERGDFSLRIEPL 161
DB 50 MRYIYLRQAPSSDSHHHEFLALWDSAKGTIRGEVEOEKIAVFRDA---SRFILNLTSV 106
QY 162 EVADEGTYSCHLHHHYHVCGLHERRVPHLTVAEPHAEPPPPRGSP-----GNGSSHS 210
DB 107 KPEDSGIYFCMI-----VGSPELTGKGTQLSVVDPLPT 140
QY 211 -GAPGDPPTLARGHNVINIVPESRAHFQQ---LGYVLA-TLLPILLVTVLLAARRR 265
DB 141 TAQPTKKSTLKK--RVCRLRPETQKGLCPITLGLLVAGVLVLLVSLGVAIHLCRRR 198
QY 266 RGGYEYSDQ 274
DB 199 RAELRFWKQ 207

Search completed: February 13, 2004, 15:30:48
Job time : 18 secs

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OM protein - protein search, using sw model

Run on: February 13, 2004, 15:14:02 ; Search time 44 Seconds
(without alignments)
1230.131 Million cell updates/sec

Title: US-10-006-818a-77

Perfect score: 1816

Sequence: 1 MALPSRILLWKLVLQSSAV.....SPLPAKYIDLKGRKFNCK 341

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
- 4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
- 5: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
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- 14: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
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- 16: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
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- 18: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
- 19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
- 20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
- 21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
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- 23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
- 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1816	100.0	341	21	Human PR01293 prot
2	1816	100.0	341	21	Human PR01293 (UNQ)
3	1816	100.0	341	22	Protein of the inv
4	1755.5	96.7	442	22	Human protein havi
5	1755.5	96.7	442	22	Human MTC48. Homo
6	1706	93.9	384	21	Human PR01293
7	1694.5	93.3	450	22	Human PR01293
8	1367.5	75.3	442	23	Rat protein isolat
9	1362.5	75.0	442	22	Murine adipocytes-

10	1300	71.6	269	22	ABE10350	Human cDNA SEQ ID
11	1300	71.6	269	23	ABE66937	Human polypeptide
12	1006	55.4	290	21	ABE59011	Breast and ovarian
13	955	52.6	192	22	ABE10523	Human cDNA SEQ ID
14	955	52.6	192	22	AAU18028	Human immunoglobul
15	955	52.6	192	23	ABE71110	Human polypeptide
16	840	46.3	255	23	ABE72366	Murine protein iso
17	826.5	45.5	260	21	AAE36108	Mouse MTC48. Mus
18	355	19.5	247	24	ABE4671	Human SECP-23 prot
19	127	7.0	447	24	ABR39440	Human GENSET polyp
20	125.5	6.9	651	19	AAW62782	Protein encoded by
21	125	6.9	651	19	AAW62782	Human TF anti-idio
22	123	6.8	650	19	AAW82544	Human LIR-p3G2 pro
23	123	6.8	650	19	AAW82544	Leukocyte immunogl
24	122	6.7	652	19	AAW82545	Human Blys binding
25	122	6.7	652	19	AAW82545	Human LIR-18A3 pro
26	122	6.7	652	21	AAW82545	Leukocyte immunogl
27	121	6.7	652	21	AAW82545	Human Blys binding
28	120	6.6	266	23	ABG97835	Single chain antib
29	120	6.6	266	23	ABG97835	Thrombopoietin ago
30	119.5	6.6	246	21	AAV15126	Anti-murine CTLA-4
31	119.5	6.6	249	23	ABP45951	Human Blys binding
32	119	6.6	240	22	AAE46058	Human TF anti-idio
33	118.5	6.5	448	19	AAW82551	Human LIR-pbm2 pro
34	118.5	6.5	448	19	AAW82551	Human gp49 Hm18 po
35	118.5	6.5	448	21	AAW82551	Leukocyte immunogl
36	117.5	6.5	469	22	AAW41582	Human polypeptide
37	117.5	6.5	472	19	AAW69234	PCR-IV protein seq
38	117	6.4	239	22	AAE46059	Human TF anti-idio
39	116.5	6.4	244	20	AAW67118	Antibody 12E10 sin
40	116.5	6.4	328	23	AAO19049	Cell adhesion mole
41	116	6.4	253	23	ABP45591	Human Blys binding
42	115.5	6.4	249	23	ABP45607	Human Blys binding
43	115.5	6.4	251	23	ABP45535	Human Blys binding
44	115.5	6.4	533	22	AAW93372	Human polypeptide
45	115.5	6.4	534	22	AAU00906	Human B lymphocyte

ALIGNMENTS

RESULT 1

AAE24031
ID AAE24031 standard; Protein; 341 AA.
XX AAE24031;
AC AAE24031;
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XX
XX 25-JAN-2001 (first entry)
XX Human PR01293 protein sequence SEQ ID NO:31.
XX Human; tumour; diagnosis; neoplastic disease; proliferation; cancer;
XX identification; tumorigenesis; anticancer; detection.

Sequence, A, Comparison

Botstein D, Goddard A, Gurney AL, Roy MA, Watanabe CK, Wood WI;
WPI; 2000-594320/56.

See over

Sequence, A,

DR N-PSDB; AAC58113.
XX
XX Antibodies specific for PRO polypeptides, used to diagnose and inhibit
PT the growth of tumors in mammals, and to identify inhibitors of PRO
PT polypeptide activity or expression -
XX
XX Claim 61; Fig 22; 226pp; English.
XX
XX The present invention describes an antibody that binds to a human
CC protein (I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780;
CC PRO3434; PRO1293; PRO1295; PRO1367; PRO1369; PRO1369; PRO1369;
CC PRO4397; PRO4407; PRO1555; PRO1096; PRO2038; and PRO2262. (I) has
CC anticancer activity and can be used to diagnose tumors in mammals, by
CC detecting complex formation when the antibody is contacted with test
CC cells. Increased expression of genes encoding (I) can also be detected
CC to diagnose tumors. Agents which inhibit the activity of (I),
CC especially the antibodies, or an antisense oligonucleotide which
CC hybridises to genes encoding (I), can be used to inhibit tumour growth,
CC preferably by inducing cell death. Methods from the present invention
CC can be used to identify compounds which inhibit the biological activity
CC of (I). AAC58102 represents PCR primers and hybridisation
CC probes used in examples from the present invention for human PRO
CC sequences. AAC58103 to AAC58122 and AAB24021 to AAB24040 represent human
CC PRO polynucleotide and protein sequences given in the exemplification of
CC the present invention.
XX

Query Match 100.0%; Score 1816; DB 21; Length 341;
Best Local Similarity 100.0%; Pred. No. 4.8e-155;
Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2
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ID AAAY99362 standard; Protein; 341 AA.
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XX AAAY99362;
AC
DT 08-AUG-2000 (first entry)
XX Human PRO1293 (UNQ662) amino acid sequence SEQ ID NO:77.
XX Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
KW transmembrane; secretion; immunoadhesion; pharmaceutical; screening.
XX Homo sapiens.
XX WO200012708-A2.
PN

XX 09-MAR-2000.
XX 01-SEP-1999;
PF 99WO-US20111.
XX 01-SEP-1998;
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PR 98US-0103328.

Sequence, A,

DR	N-PSDB; AAC58113.	
XX	Antibodies specific for PRO polypeptides, used to diagnose and inhibit	
PT	the growth of tumors in mammals, and to identify inhibitors of PRO	
PT	polypeptide activity or expression -	
XX	Claim 61; Fig 22; 226pp; English.	
XX	The present invention describes an antibody that binds to a human	
CC	protein (I) selected from: PRO1381; PRO1269; PRO1410; PRO1755; PRO1780;	
CC	PRO3434; PRO3267; PRO3267; PRO1293; PRO1303; PRO4344; PRO4354;	
CC	PRO4397; PRO4407; PRO1555; PRO1096; PRO2262. (I) has	
CC	anticancer activity and can be used to diagnose tumours in mammals, by	
CC	detecting complex formation when the antibody is contacted with test	
CC	cells. Increased expression of genes encoding (I) can also be detected	
CC	to diagnose tumours. Agents which inhibit the activity of (I),	
CC	especially the antibodies, or an antisense oligonucleotide which	
CC	hybridises to genes encoding (I), can be used to inhibit tumour growth,	
CC	preferably by inducing cell death. Methods from the present invention	
CC	can be used to identify compounds which inhibit the biological activity	
CC	of (I). AAC58019 to AAC58102 represent PCR primers and hybridisation	
CC	probes used in examples from the present invention for human PRO	
CC	sequences. AAC58103 to AAC58122 and AAC58123 to AAC58140 represent human	
CC	PRO polynucleotide and protein sequences given in the exemplification of	
CC	the present invention.	
XX	Sequence 341 AA;	
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Query Match 100.0%; Score 1816; DB 21; Length 341;		
Best Local Similarity 100.0%; Fred. No. 4.8e-155;		
Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 MALPSRILLKVLVLQSSAVLLHSVAETDAGLYTCLNLRHHYCHLYESLAVRLEVTGPP 60	
DB	1 MALPSRILLKVLVLQSSAVLLHSVAETDAGLYTCLNLRHHYCHLYESLAVRLEVTGPP 60	
QY	61 ATPAYWDEKEVLAARGAPALLTCVNRGHVWTDHVEAQQVWHDROPGVPHDADR 120	
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QY	121 LLDLYASGERRAYGLFLRDVAVGADAFERGFSLRIEPLVADDEGTYSCHLHHYCG 180	
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QY	181 HERRVHFLTVAPHAEPPTGSGSHSGAGPDPTLARGHNVINIVPESRAHFFQ 240	
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RESULT 2		
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ID	AAAY9362 standard; Protein; 341 AA.	
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AC	AAAY9362;	
DT	08-AUG-2000 (first entry)	
XX	Human PRO1293 (UNQ662) amino acid sequence SEQ ID NO:77.	
XX	Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;	
KW	transmembrane; secretion; immunoadhesion; pharmaceutical; screening.	
XX	Homo sapiens.	
XX	WO200012708-A2.	
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XX	02-SEP-1998;	98US-0099200.
XX	02-SEP-1998;	98US-0099201.
XX	02-SEP-1998;	98US-0099202.
XX	02-SEP-1998;	98US-0099203.
XX	02-SEP-1998;	98US-0099204.
XX	02-SEP-1998;	98US-0099205.
XX	02-SEP-1998;	98US-0099206.
XX	02-SEP-1998;	98US-0099207.
XX	02-SEP-1998;	98US-0099208.
XX	02-SEP-1998;	98US-0099209.
XX	02-SEP-1998;	98US-0099210.
XX	02-SEP-1998;	98US-0099211.
XX	02-SEP-1998;	98US-0099212.
XX	02-SEP-1998;	98US-0099213.
XX	02-SEP-1998;	98US-0099214.
XX	02-SEP-1998;	98US-0099215.
XX	02-SEP-1998;	98US-0099216.
XX	02-SEP-1998;	98US-0099217.
XX	02-SEP-1998;	98US-0099218.
XX	02-SEP-1998;	98US-0099219.

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OM protein - protein search, using sw model

Run on: February 13, 2004, 15:14:02 ; Search time 44 Seconds

(without alignments)
1230.131 Million cell updates/sec

Title: US-10-006-818a-77

Perfect score: 1816

Sequence: 1 MALPSRILLKLVLLQSSAV.....SPLPAKYIDLDGPKENCK 341

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 19Jun03.*

- 1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
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- 23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
- 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1816	100.0	341	21	Human PRO1293 prot
2	1816	100.0	341	21	Human PRO1293 (UNQ)
3	1816	100.0	341	22	Protein of the inv
4	1755.5	96.7	442	22	Human protein havi
5	1755.5	96.7	442	22	Human SECP-4 prote
6	1706	93.9	384	21	Human MTC48. Homo
7	1694.5	93.3	450	22	Human protein sequ
8	1367.5	75.3	442	23	Rat protein isolat
9	1362.5	75.0	442	22	Murine adipocytes-

10	1300	71.6	269	22	ABE10350	Human cDNA SEQ ID
11	1300	71.6	269	23	ABP66937	Human polypeptide
12	1006	55.4	290	21	AAE59011	Breast and ovarian
13	955	52.6	192	22	ABE10523	Human cDNA SEQ ID
14	955	52.6	192	22	AAU18028	Human immunoglobul
15	955	52.6	192	23	ABP67110	Human polypeptide
16	840	46.3	253	23	ABP72366	Murine protein iso
17	826.5	45.5	260	21	AAE36108	Mouse MIC48. Mus
18	355	19.5	218	24	ABE84671	Human SEC23 prot
19	127	7.0	447	24	ABK39440	Human GENSET poly
20	125.5	6.9	651	19	AAW62782	Protein encoded by
21	125	6.9	244	22	AAE46060	Human TF anti-idio
22	123	6.8	650	19	AAW82544	Human LIR-P3G2 pro
23	123	6.8	650	21	AAE04169	Leukocyte immunogl
24	122	6.7	253	23	ABP45328	Human BLYS binding
25	122	6.7	652	19	AAE82548	Human LIR-18A3 pro
26	122	6.7	652	21	AAE04170	Leukocyte immunogl
27	121	6.7	254	23	ABP45955	Human BLYS binding
28	120	6.6	266	23	ABG97835	Single chain antib
29	120	6.6	266	23	ABG35336	Thrombopoietin ago
30	119.5	6.6	246	21	AAE15126	Anti-murine CTLA-4
31	119.5	6.6	249	23	ABP45951	Human BLYS binding
32	119	6.6	240	22	ABP46058	Human TF anti-idio
33	118.5	6.5	448	19	AAE82551	Human LIR-pbm2 pro
34	118.5	6.5	448	19	AAE53463	Human gp49 Hm18 po
35	118.5	6.5	448	21	AAE04176	Leukocyte immunogl
36	117.5	6.5	469	22	AAE41582	Human polypeptide
37	117.5	6.5	472	19	AAE69234	FCR-IV protein seq
38	117	6.4	239	22	AAE46059	Human TF anti-idio
39	116.5	6.4	244	20	AAE06718	Antibody 12E10 sin
40	116.5	6.4	328	23	AAE19049	Cell adhesion mole
41	116	6.4	253	23	ABP45591	Human BLYS binding
42	115.5	6.4	249	23	ABP45607	Human BLYS binding
43	115.5	6.4	251	23	ABP45535	Human BLYS binding
44	115.5	6.4	533	22	AAE93372	Human polypeptide
45	115.5	6.4	534	22	AAU00906	Human B lymphocyte

ALIGNMENTS

RESULT 1

AAE24031

ID AAE24031 standard; Protein; 341 AA.

XX AC AAE24031;

XX DT 25-JAN-2001 (first entry)

XX DE Human PRO1293 protein sequence SEQ ID NO:31.

XX KW Human; tumour; diagnosis; neoplastic disease; proliferation; cancer;

XX KW identification; tumorigenesis; anticancer; detection.

XX OS Homo sapiens.

XX PN WO200053750-A1.

XX PD 14-SEP-2000

XX PF 02-DEC-1999; 99WO-US28551.

XX PR 08-MAR-1999; 99WO-US05028.

XX PR 01-SEP-1999; 99WO-US20111.

XX PR 29-OCT-1999; 99US-0162506.

XX PR 30-NOV-1999; 99WO-US28313.

XX PR 01-DEC-1999; 99WO-US28634.

XX PA (GETH) GENENTECH INC.

XX PI Botstein D, Goddard A, Gurney AL, Roy NA, Watanabe CK, Wood WI;

XX WPI; 2000-594320/56.

Sequence, A, Comparison

See over